(PTZ), one of the convulsant drugs (Shimizu-Nishikawa *et al.*, 1995, Brain Res Mol Brain Res 28(2):201-10, PMID: 7723619). Thus, SEZ-6 protein encoded by this gene may also play a role in brain seizure.

In addition, moderate to low levels of expression of this gene is also seen in three lung cancer cell lines and two of the glioma cell lines. Therefore, expression of this gene may be used as diagnostic marker to detect lung cancer and glioma. Furthermore, modulation of this gene or its protein product through the use of antibody or protein therapeutics, may be useful in the treatment of lung cancer and glioma.

Panel 2D Summary: Ag2795/Ag2807 Two experiments with same probe and primer sets are in excellent agreement with highest expression of this gene detected in liver cancer 1026 sample (CTs=31.3). In addition, moderate to low levels of expression of this gene is also seen in a lung cancer and a liver cancer (6005-T). Expression of this gene is higher in cancer as compared to corresponding adjacent normal tissue (CTs>37). Thus, expression of this gene may be used to distinguish between normal and cancer samples and as diagnostic marker to detect lung and liver cancer. In addition, therapeutic modulation of this gene through the use of antibodies may be useful in the treatment of these cancers.

Panel 4.1D Summary: Ag7017 Low levels of expression of this gene is restricted to TNF alpha and LPS stimulated neutrophils (CT=34.4). Therefore, expression of this gene may be used to distinguish this sample from other samples in the panel. This expression profile suggest that the protein encoded by this gene is produced by activated neutrophils but not by resting neutrophils. Therefore, therapeutic modulation of this gene product through the use of antibodies or small molecule drug may reduce activation of these inflammatory cells and be useful to reduce or eliminate the symptoms in patients with Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis. In addition, small molecule or antibody antagonists of this gene product may be effective in increasing the immune response in patients with AIDS or other immunodeficiencies.

Panel 4D Summary: Ag2807 Highest expression of this gene is detected in astrocytes (CTs=33). Thus expression of this gene may be used to distinguish astrocytes from other samples in this panel. In addition, low but significant levels of expression of this gene is also seen in normal tissue represented by colon and kidney. Therefore, therapeutic modulation of this gene may be useful in the treatment of autoimmune and inflammatory

diseases affecting brain, colon and kidney such as lupus erythematosus, Crohn's disease, and ulcerative colitis.

general oncology screening panel_v_2.4 Summary: Ag2795 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

AH. CG52919-05 and CG52919-06: SEZ-6-Like Protein (7520500-54-4).

Expression of gene CG52919-05 and CG52919-06 was assessed using the primer-probe sets Ag2796, Ag90 and Ag124, described in Tables AHA, AHB and AHC. Results of the RTQ-PCR runs are shown in Tables AHD, AHE, AHF and AHG. Note that probe-primer sets Ag2796 and Ag124 are specific for the CG52919-05 variant. Also, Note that CG52919-06 represents a full-length physical clone.

Table AHA. Probe Name Ag2796

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctacaaccgcattaccataga-3'	22	1670	399
Probe	TET-5'-tcagcgtttgacaatccaacttacga-3'-TAMRA	26	1693	400
Reverse	5'-gtctcctgcaaaggaaagagat-3'	22	1725	401

Table AHB. Probe Name Ag90

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttggcctggactgcttcttc-3'	20	977	402
Probe	TET-5'-catctctgtctaccctggctatggcgtg-3'-TAMRA	28	999	403
Reverse	5'-aggctgatattctggaccttgatt-3'	24	1029	404

Table AHC. Probe Name Ag124

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cgcccctacaaccgcat-3'	17	1666	405

498

Probe	TET-5'-ccatagagtcagcgtttgacaatccaacttacg-3'-TAMRA	33	1685	406
Reverse	5'-ctgcaaaggaaagagatccagtc-3'	23	1719	407

Table AHD. Panel 1

Tissue Name	Rel. Exp.(%) Ag124, Run 87587871	Rel. Exp.(%) Ag90, Run 87586258	Tissue Name	Rel. Exp.(%) Ag124, Run 87587871	Rel. Exp.(%) Ag90, Run 87586258
Endothelial cells	0.0	0.0	Renal ca. 786-0	0.0	0.0
Endothelial cells (treated)	0.0	0.0	Renal ca. A498	0.0	0.0
Pancreas	0.1	0.1	Renal ca. RXF 393	0.0	0.0
Pancreatic ca. CAPAN 2	0.0	0.0	Renal ca. ACHN	0.0	0.0
Adrenal gland	0.0	0.0	Renal ca. UO-31	0.0	0.0
Thyroid	0.0	0.0	Renal ca. TK-10	0.0	0.0
Salivary gland	0.0	0.0	Liver	0.0	0.0
Pituitary gland	0.0	0.0	Liver (fetal)	0.0	0.0
Brain (fetal)	25.3	37.1	Liver ca. (hepatoblast) HepG2	0.0	0.0
Brain (whole)	24.0	22.5	Lung	0.0	0.0
Brain (amygdala)	26.2	24.8	Lung (fetal)	0.0	0.0
Brain (cerebellum)	**100.0**	**100.0**	Lung ca. (small cell) LX-1	0.0	0.0
Brain (hippocampus)	21.6	29.5	Lung ca. (small cell) NCI-H69	43.5	33.7
Brain (substantia nigra)	7.7	7.6	Lung ca. (s.cell var.) SHP-77	0.0	0.0
Brain (thalamus)	20.0	13.7	Lung ca. (large cell)NCI-H460	0.0	0.0
Brain (hypothalamus)	8.4	7.7	Lung ca. (non-sm. cell) A549	0.0	0.0
Spinal cord	1.8	1.4	Lung ca. (non-s.cell) NCI-H23	0.0	0.0

glio/astro U87-MG	0.0	0.0	Lung ca. (non-s.cell) HOP-62	0.0	0.0
glio/astro U-118-MG	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	0.0	0.0
astrocytoma SW1783	0.0	0.0	Lung ca. (squam.) SW 900	0.0	0.0
neuro*; met SK-N-AS	0.0	0.4	Lung ca. (squam.) NCI-H596	26.8	20.0
astrocytoma SF-539	0.0	0.0	Mammary gland	0.0	0.1
astrocytoma SNB-75	0.0	0.0	Breast ca.* (pl.ef) MCF-7	0.0	0.0
glioma SNB-19	2.1	1.8	Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0
glioma U251	0.5	0.4	Breast ca.* (pl. ef) T47D	0.0	0.0
glioma SF-295	0.0	0.0	Breast ca. BT-549	0.0	0.0
Heart	0.0	0.0	Breast ca. MDA-N	0.0	0.0
Skeletal muscle	0.0	0.0	Ovary	0.0	0.0
Bone marrow	0.0	0.0	Ovarian ca. OVCAR-3	0.0	0.0
Thymus	0.0	0.1	Ovarian ca. OVCAR-4	0.0	0.0
Spleen	0.0	0.0	Ovarian ca. OVCAR-5	0.0	0.0
Lymph node	0.0	0.0	Ovarian ca. OVCAR-8	0.0	0.0
Colon (ascending)	0.0	0.1	Ovarian ca. IGROV-1	0.0	0.0
Stomach	0.0	0.1	Ovarian ca. (ascites) SK-OV-3	0.0	0.0
Small intestine	0.5	0.3	Uterus	0.0	0.0
Colon ca. SW480	0.0	0.0	Placenta	0.0	0.0
Colon ca.* SW620 (SW480 met)	0.0	0.0	Prostate	0.0	0.0
Colon ca. HT29	0.0	0.0	Prostate ca.* (bone met) PC-3	0.0	0.0
Colon ca. HCT-116	0.0	0.0	Testis	1.0	1.3

Colon ca. CaCo-2	0.0	0.0	Melanoma Hs688(A).T	0.0	0.0
Colon ca. HCT-15	0.0	0.0	Melanoma* (met) Hs688(B).T	0.0	0.0
Colon ca. HCC-2998	0.0	0.0	Melanoma UACC-62	0.0	0.0
Gastric ca. * (liver met) NCI-N87	0.0	0.0	Melanoma M14	0.0	0.0
Bladder	0.0	0.0	Melanoma LOX IMVI	0.0	0.0
Trachea	0.0	0.0	Melanoma* (met) SK-MEL-5	0.0	0.0
Kidney	0.0	0.0	Melanoma SK-MEL-28	0.0	0.0
Kidney (fetal)	0.0	0.0			

Table AHE. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag2796, Run 165527192	Tissue Name	Rel. Exp.(%) Ag2796, Run 165527192
Liver adenocarcinoma	0.0	Kidney (fetal)	0.0
Pancreas	0.0	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	0.4
Adrenal gland	0.2	Renal ca. RXF 393	0.0
Thyroid	0.0	Renal ca. ACHN	0.2
Salivary gland	0.0	Renal ca. UO-31	0.0
Pituitary gland	10.0	Renal ca. TK-10	0.0
Brain (fetal)	**100.0**	Liver	0.0
Brain (whole)	65.1	Liver (fetal)	0.0
Brain (amygdala)	76.8	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	76.8	Lung	0.0
Brain (hippocampus)	51.4	Lung (fetal)	0.0
Brain (substantia nigra)	11.7	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	70.2	Lung ca. (small cell) NCI-H69	23.8

Cerebral Cortex	37.9	Lung ca. (s.cell var.) SHP-77	21.6
Spinal cord	3.5	Lung ca. (large cell)NCI-H460	0.6
glio/astro U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.0
glio/astro U-118-MG	0.1	Lung ca. (non-s.cell) NCI-H23	0.0
astrocytoma SW1783	0.0	Lung ca. (non-s.cell) HOP-62	0.0
neuro*; met SK-N-AS	0.4	Lung ca. (non-s.cl) NCI-H522	0.0
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	0.1
astrocytoma SNB-75	0.0	Lung ca. (squam.) NCI-H596	35.8
glioma SNB-19	3.2	Mammary gland	0.0
glioma U251	4.3	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	0.1
Heart (fetal)	0.0	Breast ca.* (pl.ef) T47D	0.0
Heart	0.0	Breast ca. BT-549	0.1
Skeletal muscle (fetal)	2.3	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	0.0	Ovarian ca. OVCAR-3	0.0
Thymus	0.0	Ovarian ca. OVCAR-4	0.0
Spleen	0.1	Ovarian ca. OVCAR-5	0.1
Lymph node	0.3	Ovarian ca. OVCAR-8	0.0
Colorectal	0.0	Ovarian ca. IGROV-1	0.0
Stomach	0.1	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	0.6	Uterus	0.1
Colon ca. SW480	0.0	Placenta	1.9
Colon ca.* SW620(SW480 met)	0.0	Prostate	0.0

Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	3.3	Testis	2.0
Colon ca. CaCo-2	0.0	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	0.0	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	0.0	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	0.0	Melanoma M14	0.0
Bladder	0.0	Melanoma LOX IMVI	0.0
Trachea	0.0	Melanoma* (met) SK-MEL-5	0.0
Kidney	0.0	Adipose	0.0

Table AHF. Panel 2D

Tissue Name	Rel. Exp.(%) Ag2796, Run 162570140	Tissue Name	Rel. Exp.(%) Ag2796, Run 162570140
Normal Colon	26.6	Kidney Margin 8120608	0.0
CC Well to Mod Diff (ODO3866)	0.0	Kidney Cancer 8120613	0.0
CC Margin (ODO3866)	4.2	Kidney Margin 8120614	1.7
CC Gr.2 rectosigmoid (ODO3868)	0.0	Kidney Cancer 9010320	3.5
CC Margin (ODO3868)	0.7	Kidney Margin 9010321	3.7
CC Mod Diff (ODO3920)	0.0	Normal Uterus	3.7
CC Margin (ODO3920)	13.1	Uterus Cancer 064011	6.0
CC Gr.2 ascend colon (ODO3921)	4.8	Normal Thyroid	0.0
CC Margin (ODO3921)	5.1	Thyroid Cancer 064010	0.0
CC from Partial Hepatectomy (ODO4309) Mets	8.5	Thyroid Cancer A302152	3.5
Liver Margin (ODO4309)	0.0	Thyroid Margin A302153	0.0
Colon mets to lung (OD04451-01)	0.0	Normal Breast	4.5

Lung Margin (OD04451-02)	1.1	Breast Cancer (OD04566)	1.8
Normal Prostate 6546-1	17.6	Breast Cancer (OD04590-01)	3.0
Prostate Cancer (OD04410)	12.3	Breast Cancer Mets (OD04590-03)	6.3
Prostate Margin (OD04410)	6.2	Breast Cancer Metastasis (OD04655-05)	9.2
Prostate Cancer (OD04720-01)	11.5	Breast Cancer 064006	2.3
Prostate Margin (OD04720-02)	18.3	Breast Cancer 1024	4.3
Normal Lung 061010	2.0	Breast Cancer 9100266	4.1
Lung Met to Muscle (ODO4286)	0.0	Breast Margin 9100265	0.0
Muscle Margin (ODO4286)	0.7	Breast Cancer A209073	3.0
Lung Malignant Cancer (OD03126)	1.0	Breast Margin A209073	0.7
Lung Margin (OD03126)	2.1	Normal Liver	0.0
Lung Cancer (OD04404)	1.8	Liver Cancer 064003	0.0
Lung Margin (OD04404)	2.1	Liver Cancer 1025	3.7
Lung Cancer (OD04565)	5.6	Liver Cancer 1026	95.9
Lung Margin (OD04565)	0.0	Liver Cancer 6004-T	0.0
Lung Cancer (OD04237-01)	48.0	Liver Tissue 6004-N	7.2
Lung Margin (OD04237-02)	0.0	Liver Cancer 6005-T	100.0
Ocular Mel Met to Liver (ODO4310)	2.8	Liver Tissue 6005-N	0.0
Liver Margin (ODO4310)	0.0	Normal Bladder	8.8
Melanoma Mets to Lung (OD04321)	1.3	Bladder Cancer 1023	0.0
Lung Margin (OD04321)	21.6	Bladder Cancer A302173	1.5
Normal Kidney	6.9	Bladder Cancer (OD04718-01)	1.8
Kidney Ca, Nuclear grade 2 (OD04338)	6.4	Bladder Normal Adjacent (OD04718-03)	2.8
Kidney Margin (OD04338)	2.0	Normal Ovary	4.9

Kidney Ca Nuclear grade 1/2 (OD04339)	0.9	Ovarian Cancer 064008	3.6
Kidney Margin (OD04339)	3.0	Ovarian Cancer (OD04768-07)	2.5
Kidney Ca, Clear cell type (OD04340)	3.0	Ovary Margin (OD04768-08)	0.0
Kidney Margin (OD04340)	1.3	Normal Stomach	3.7
Kidney Ca, Nuclear grade 3 (OD04348)	0.7	Gastric Cancer 9060358	0.6
Kidney Margin (OD04348)	2.5	Stomach Margin 9060359	4.8
Kidney Cancer (OD04622-01)	0.8	Gastric Cancer 9060395	1.8
Kidney Margin (OD04622-03)	0.0	Stomach Margin 9060394	1.0
Kidney Cancer (OD04450-01)	3.9	Gastric Cancer 9060397	0.0
Kidney Margin (OD04450-03)	2.2	Stomach Margin 9060396	1.0
Kidney Cancer 8120607	0.8	Gastric Cancer 064005	5.3

Table AHG. Panel 4D

Tissue Name	Rel. Exp.(%) Ag2796, Run 162292586	Tissue Name	Rel. Exp.(%) Ag2796, Run 162292586
Secondary Th1 act	4.3	HUVEC IL-1beta	0.0
Secondary Th2 act	8.9	HUVEC IFN gamma	8.1
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	4.7
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	4.2
Secondary Tr1 rest	4.7	Lung Microvascular EC none	3.7
Primary Th1 act	6.2	Lung Microvascular EC TNFalpha + IL-1beta	3.7
Primary Th2 act	0.0	Microvascular Dermal EC none	9.9
Primary Tr1 act	4.0	Microsvasular Dermal EC TNFalpha + IL-1beta	4.2

Primary Th1 rest	4.1	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	8.2	Coronery artery SMC rest	0.0
CD45RO CD4 lymphocyte act	6.0	Coronery artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	8.4	Astrocytes rest	34.9
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	42.3
Secondary CD8 lymphocyte act	9.5	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	14.2
2ry Th1/Th2/Tr1_anti-CD95 CH11	14.5	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	16.8	Liver cirrhosis	3.8
LAK cells IL-2+IL-12	3.8	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	3.9	NCI-H292 none	30.6
LAK cells IL-2+ IL-18	21.8	NCI-H292 IL-4	15.3
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	30.1
NK Cells IL-2 rest	15.4	NCI-H292 IL-13	18.2
Two Way MLR 3 day	18.8	NCI-H292 IFN gamma	8.3
Two Way MLR 5 day	7.9	HPAEC none	0.0
Two Way MLR 7 day	3.1	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	6.1	Lung fibroblast none	11.2
PBMC PWM	20.4	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	6.5	Lung fibroblast IL-4	7.5

Ramos (B cell) none	3.3	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	23.0	Lung fibroblast IL-13	4.2
B lymphocytes PWM	35.6	Lung fibroblast IFN gamma	9.5
B lymphocytes CD40L and IL-4	70.7	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	7.4	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	51.1	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	10.6	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	20.9	Dermal fibroblast IL-4	8.9
Dendritic cells anti-CD40	9.8	IBD Colitis 2	0.0
Monocytes rest	9.3	IBD Crohn's	0.0
Monocytes LPS	9.6	Colon	100.0
Macrophages rest	4.6	Lung	17.2
Macrophages LPS	5.4	Thymus	20.3
HUVEC none	11.3	Kidney	33.0
HUVEC starved	18.4		

Panel 1 Summary: Ag90/Ag2796 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in brain cerebellum (CT=25-26). High levels of expression of this gene is mainly seen in all the regions of brain including amygdala, hippocampus, substantia nigra, thalamus, cerebellum,

5   cerebral cortex, and spinal cord. In addition, moderate levels of expression of this gene is also seen in two lung cancer cell lines and a glioma cell line. See panel 1.3D for further discussion of this gene.

Panel 1.3D Summary: Ag2796 Highest expression of this gene is detected in fetal brain (CT=28.7). Moderate levels of expression of this gene is mainly seen in all the regions

10   of brain including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene codes for a homolog of mouse seizure related protein, SEZ-6. Mouse SEZ-6 was first isolated from cerebrum cortex-derived cells treated with pentylentetrazole (PTZ), one of the convulsant drugs (Shimizu-Nishikawa *et al.*, 1995, Brain Res Mol Brain Res 28(2):201-10, PMID: 7723619). Thus, SEZ-6 protein encoded by this gene may also

5   play a role in brain seizure.

In addition, moderate to low levels of expression of this gene is also seen in three lung cancer cell lines, two of the glioma cell lines and a colon cancer cell line. Therefore, expression of this gene may be used as diagnostic marker to detect lung, colon and brain cancers. Furthermore, modulation of this gene or its protein product through the use of

10   antibody or protein therapeutics, may be useful in the treatment of lung, colon and brain cancers.

Significant expression is also detected in fetal skeletal muscle. This gene is expressed at much higher levels in fetal (CT = 34.1) when compared to adult skeletal muscle (CT = 40). This observation suggests that expression of this gene can be used to

15   distinguish fetal from adult skeletal muscle. In addition, the relative overexpression of this gene in fetal skeletal muscle suggests that the protein product may enhance muscular growth or development in the fetus and thus may also act in a regenerative capacity in the adult. Therefore, therapeutic modulation of the SEZ-6 encoded by this gene could be useful in treatment of muscle related diseases. More specifically, treatment of weak or dystrophic

20   muscle with the protein encoded by this gene could restore muscle mass or function.

Panel 2D Summary: Ag2796 Highest expression of this gene is detected in two liver cancer samples (CTs=32.3). In addition, low levels of expression of this gene is also seen in a lung cancer sample. Expression of this gene is higher in lung and liver cancer as compared to corresponding adjacent normal tissue (CTs=40). Thus, expression of this gene

25   may be used to distinguish between normal and cancer samples and as diagnostic marker to detect lung and liver cancer. In addition, therapeutic modulation of this gene through the use of antibodies may be useful in the treatment of these cancers.

Panel 4D Summary: Ag2796 Low but significant expression of this gene is detected exclusively in colon (CT=34.8). Therefore, expression of this gene may be used to

30   distinguish colon from the other tissues on this panel. Furthermore, expression of this gene is decreased in colon samples from patients with inflammatory bowel disease, colitis and Crohn's disease relative to normal colon. Therefore, therapeutic modulation of the activity

of the SEZ-6 protein encoded by this gene may be useful in the treatment of inflammatory bowel disease.

AI. CG55698-02: Colipase precursor protein-like protein.

Expression of gene CG55698-02 was assessed using the primer-probe set Ag7086, described in Table AIA. Results of the RTQ-PCR runs are shown in Table AIB. Note that CG55698-02 represents a full-length physical clone.

Table AIA. Probe Name Ag7086

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'- cattatcaacctgacgctctatg-3'	23	88	408
Probe	TET-5'- ccacgctcacagggacacttgtagta -3'-TAMRA	26	116	409
Reverse	5'-atggtcttgtctccctcaca-3'	20	149	410

Table AIB. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag7086, Run 296433065	Tissue Name	Rel. Exp.(%) Ag7086, Run 296433065
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	12.1
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0

Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0

Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.4	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	100.0

CNS_neurodegeneration_v1.0 Summary: Ag7086 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.6 Summary: Ag7086 Highest expression of this gene is seen in pancreas (CT=22.7). Therefore, expression of this gene may be used to distinguish pancrease from other samples in this panel. This gene codes for a deletion variant of colipase. Pancreatic colipase is a 12-kD polypeptide cofactor for pancreatic lipase, an enzyme essential for the absorption of dietary long-chain triglyceride fatty acids. Colipase is thought to anchor lipase noncovalently to the surface of lipid micelles, counteracting the destabilizing influence of intestinal bile salts (OMIM 120105). Therefore, therapeutic modulation of expression of this gene or colipase encoded by this gene may be useful in the treatment of dietary fat related disorders including pancreatic insufficiency and fat malabsorption.

AJ. CG55832-02 and CG55832-03: Tenascin-C Precursor Protein-like Protein.

Expression of gene CG55832-02 and CG55832-03 was assessed using the primer-probe set Ag4681, described in Table AJA. Results of the RTQ-PCR runs are shown in Tables AJB, AJC and AJD.

Table AJA. Probe Name Ag4681

Primers	Sequences	Length	Start Position	SEQ ID No

Forward	5'-tgttccaaagagccaacaag-3'	20	2868	411
Probe	TET-5'-ccaaaaccacactcacaggtctgagg-3'-TAMRA	26	2894	412
Reverse	5'-agcagaaactccaatcccatat-3'	22	2931	413

Table AJB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4681, Run 222811927	Tissue Name	Rel. Exp.(%) Ag4681, Run 222811927
Adipose	0.9	Renal ca. TK-10	0.4
Melanoma* Hs688(A).T	18.2	Bladder	1.3
Melanoma* Hs688(B).T	7.3	Gastric ca. (liver met.) NCI-N87	1.3
Melanoma* M14	10.8	Gastric ca. KATO III	0.3
Melanoma* LOXIMVI	7.7	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	3.8	Colon ca. SW480	0.2
Squamous cell carcinoma SCC-4	1.2	Colon ca.* (SW480 met) SW620	6.7
Testis Pool	1.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	7.7	Colon ca. HCT-116	0.0
Prostate Pool	1.7	Colon ca. CaCo-2	0.3
Placenta	0.1	Colon cancer tissue	3.7
Uterus Pool	2.5	Colon ca. SW1116	0.1
Ovarian ca. OVCAR-3	3.2	Colon ca. Colo-205	0.3
Ovarian ca. SK-OV-3	0.2	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.5	Colon Pool	5.9
Ovarian ca. OVCAR-5	0.2	Small Intestine Pool	3.4
Ovarian ca. IGROV-1	13.9	Stomach Pool	2.9
Ovarian ca. OVCAR-8	4.6	Bone Marrow Pool	2.9
Ovary	0.2	Fetal Heart	0.1
Breast ca. MCF-7	0.0	Heart Pool	3.7
Breast ca. MDA-MB-231	2.6	Lymph Node Pool	7.9

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Breast ca. BT 549	2.4	Fetal Skeletal Muscle	0.4
Breast ca. T47D	0.4	Skeletal Muscle Pool	1.0
Breast ca. MDA-N	3.7	Spleen Pool	2.0
Breast Pool	4.5	Thymus Pool	2.5
Trachea	3.1	CNS cancer (glio/astro) U87-MG	29.1
Lung	0.1	CNS cancer (glio/astro) U-118-MG	**100.0**
Fetal Lung	8.7	CNS cancer (neuro;met) SK-N-AS	0.9
Lung ca. NCI-N417	0.2	CNS cancer (astro) SF-539	3.6
Lung ca. LX-1	3.6	CNS cancer (astro) SNB-75	37.4
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	13.1
Lung ca. SHP-77	1.0	CNS cancer (glio) SF-295	8.2
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.4
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.3
Lung ca. NCI-H23	0.1	Brain (fetal)	3.4
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.4
Lung ca. HOP-62	11.8	Cerebral Cortex Pool	0.4
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.5
Liver	0.1	Brain (Thalamus) Pool	0.7
Fetal Liver	0.2	Brain (whole)	0.9
Liver ca. HepG2	0.0	Spinal Cord Pool	1.0
Kidney Pool	11.3	Adrenal Gland	0.4
Fetal Kidney	7.1	Pituitary gland Pool	0.2
Renal ca. 786-0	2.2	Salivary Gland	0.3
Renal ca. A498	0.3	Thyroid (female)	0.1
Renal ca. ACHN	0.5	Pancreatic ca. CAPAN2	0.4
Renal ca. UO-31	1.3	Pancreas Pool	3.5

Table AJC. Oncology_cell_line_screening_panel_v3.1

Tissue Name	Rel. Exp.(%) Ag4681, Run 224056814	Tissue Name	Rel. Exp.(%) Ag4681, Run 224056814
Daoy Medulloblastoma/Cerebellum	8.6	Ca Ski_Cervical epidermoid carcinoma (metastasis)	18.7
TE671 Medulloblastom/Cerebellum	9.2	ES-2_Ovarian clear cell carcinoma	6.0
D283 Med Medulloblastoma/Cerebellum	0.1	Ramos/6h stim_ Stimulated with PMA/ionomycin 6h	0.0
PFSK-1 Primitive Neuroectodermal/Cerebellum	4.4	Ramos/14h stim_ Stimulated with PMA/ionomycin 14h	0.0
XF-498_CNS	**100.0**	MEG-01_Chronic myelogenous leukemia (megokaryoblast)	0.0
SNB-78_CNS/glioma	66.4	Raji_Burkitt's lymphoma	0.0
SF-268_CNS/glioblastoma	2.0	Daudi_Burkitt's lymphoma	0.0
T98G_Glioblastoma	5.0	U266_B-cell plasmacytoma/myeloma	0.0
SK-N-SH_Neuroblastoma (metastasis)	78.5	CA46_Burkitt's lymphoma	0.0
SF-295_CNS/glioblastoma	6.4	RL_non-Hodgkin's B-cell lymphoma	0.0
Cerebellum	0.2	JM1_pre-B-cell lymphoma/leukemia	0.0
Cerebellum	0.4	Jurkat_T cell leukemia	0.0
NCI-H292_Mucoepidermoid lung ca.	1.6	TF-1_Erythroleukemia	0.0
DMS-114_Small cell lung cancer	0.4	HUT 78_T-cell lymphoma	0.0
DMS-79_Small cell lung cancer/neuroendocrine	0.2	U937_Histiocytic lymphoma	0.0
NCI-H146_Small cell lung cancer/neuroendocrine	0.0	KU-812_Myelogenous leukemia	0.0
NCI-H526_Small cell lung cancer/neuroendocrine	0.1	769-P_Clear cell renal ca.	0.0
NCI-N417_Small cell lung cancer/neuroendocrine	1.8	Caki-2_Clear cell renal ca.	0.7
NCI-H82_Small cell lung cancer/neuroendocrine	0.0	SW 839_Clear cell renal ca.	4.1

NCI-H157_Squamous cell lung cancer (metastasis)	5.6	G401_Wilms' tumor	0.0
NCI-H1155_Large cell lung cancer/neuroendocrine	0.0	Hs766T_Pancreatic ca. (LN metastasis)	0.0
NCI-H1299_Large cell lung cancer/neuroendocrine	0.3	CAPAN-1_Pancreatic adenocarcinoma (liver metastasis)	0.1
NCI-H727_Lung carcinoid	0.2	SU86.86_Pancreatic carcinoma (liver metastasis)	4.3
NCI-UMC-11_Lung carcinoid	0.0	BxPC-3_Pancreatic adenocarcinoma	0.0
LX-1_Small cell lung cancer	9.0	HPAC_Pancreatic adenocarcinoma	0.5
Colo-205_Colon cancer	1.3	MIA PaCa-2_Pancreatic ca.	0.1
KM12_Colon cancer	3.3	CFPAC-1_Pancreatic ductal adenocarcinoma	10.3
KM20L2_Colon cancer	0.2	PANC-1_Pancreatic epithelioid ductal ca.	0.9
NCI-H716_Colon cancer	0.0	T24_Bladder ca. (transitional cell)	0.1
SW-48_Colon adenocarcinoma	0.0	5637_Bladder ca.	13.8
SW1116_Colon adenocarcinoma	0.4	HT-1197_Bladder ca.	0.1
LS 174T_Colon adenocarcinoma	2.4	UM-UC-3_Bladder ca. (transitional cell)	2.9
SW-948_Colon adenocarcinoma	0.1	A204_Rhabdomyosarcoma	61.1
SW-480_Colon adenocarcinoma	0.1	HT-1080_Fibrosarcoma	1.3
NCI-SNU-5_Gastric ca.	0.2	MG-63_Osteosarcoma (bone)	2.2
KATO III_Stomach	0.2	SK-LMS-1_Leiomyosarcoma (vulva)	28.1
NCI-SNU-16_Gastric ca.	25.7	SJRH30_Rhabdomyosarcoma (met to bone marrow)	23.0
NCI-SNU-1_Gastric ca.	0.0	A431_Epidermoid ca.	0.1
RF-1_Gastric adenocarcinoma	0.0	WM266-4_Melanoma	51.1
RF-48_Gastric adenocarcinoma	0.0	DU 145_Prostate	4.5
MKN-45_Gastric ca.	0.3	MDA-MB-468_Breast adenocarcinoma	0.0
NCI-N87_Gastric ca.	0.2	SSC-4_Tongue	3.3
OVCAR-5_Ovarian ca.	0.3	SSC-9_Tongue	15.5
RL95-2_Uterine carcinoma	0.0	SSC-15_Tongue	9.9

| HelaS3_Cervical adenocarcinoma | 0.0 | CAL 27_Squamous cell ca. of tongue | 31.9 |

Table AJD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4681, Run 268722514	Tissue Name	Rel. Exp.(%) Ag4681, Run 268722514
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	8.5
Primary Th2 rest	0.0	Small airway epithelium none	3.1
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	10.2
CD45RA CD4 lymphocyte act	14.4	Coronery artery SMC rest	1.4
CD45RO CD4 lymphocyte act	0.0	Coronery artery SMC TNFalpha + IL-1beta	3.5
CD8 lymphocyte act	0.0	Astrocytes rest	9.6
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	7.7
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	15.1

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LAK cells rest	0.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	22.4
LAK cells IL-2	0.0	Liver cirrhosis	0.6
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.1
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	1.1
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.1
LAK cells PMA/ionomycin	0.4	NCI-H292 IL-13	2.2
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.1
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	0.0	Lung fibroblast none	46.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	19.8
PBMC PWM	0.0	Lung fibroblast IL-4	74.7
PBMC PHA-L	0.0	Lung fibroblast IL-9	75.3
Ramos (B cell) none	0.0	Lung fibroblast IL-13	44.4
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	53.2
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	27.7
B lymphocytes CD40L and IL-4	0.1	Dermal fibroblast CCD1070 TNF alpha	26.4
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	31.9
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	12.8
Dendritic cells none	0.6	Dermal fibroblast IL-4	100.0
Dendritic cells LPS	0.6	Dermal Fibroblasts rest	4.6
Dendritic cells anti-CD40	0.2	Neutrophils TNFa+LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.1	Colon	0.5
Macrophages rest	0.1	Lung	0.4
Macrophages LPS	0.2	Thymus	0.2

HUVEC none	0.0	Kidney	1.2
HUVEC starved	0.0		

General_screening_panel_v1.4 Summary: Ag4681 Highest expression of this gene is seen in a brain cancer cell line (CT=20.3). Prominent expression of this gene is also seen in a cluster of samples derived from brain cancer cell lines. High levels of expression are also seen in cell lines from colon, renal, ovarian, lung, breast, prostate, and melanoma

5   cancers. This gene encodes a homolog of tenascin-C, an extracellular matrix protein that appears at active sites of tissue remodelling during cancer invasion. Tenascin has been shown to be highly expressed around tumours, including invasive breast carcinomas and may be expressed by these invasive carcinomas (Adams M. Cancer Res 2002 Jun 1;62(11):3289-97). Zagzag et. al has suggested a potential role for tenascin-C in

10 pathological angiogenesis (Cancer Res 2002 May 1;62(9):2660-8). Thus, expression of this gene could be used to differentiate between these cell lines and other samples on this panel, and as a marker of brain cancer. Based on the homology of this gene to tenascin-C and the expression in brain cancer cell lines, therapeutic modulation of the expression or function of this protein may be useful in the treatment of colon, brain, renal, ovarian, lung, breast,

15 prostate, and melanoma cancers.

Oncology_cell_line_screening_panel_v3.1 Summary: Ag4681 Highest expression of this gene is seen in a brain cancer cell line (CT=23.7), consistent with expression in panel 1.4. In addition, high levels of expression are seen in other cell lines on this panel, including samples from gastric and lung cancers. See Panel 1.4 for discussion of

20 this gene in cancer.

Panel 4.1D Summary: Ag4681 Highest expression of this gene is seen in IL-4 treated dermal fibroblasts (CT=22.72). High levels of expression of this gene are seen in treated and untreated lung and dermal fibroblasts, keratinocytes, astrocytes, and bronchial and small airway epithelium. Moderate to low levels of expression of this gene is also seen

25 in naive T cells, resting and activated dendritic cells and activated B lymphocytes. Expression of this gene in dendritic cells suggests a role for this gene in antigen presentation. This gene has homology to tenascin-C, an extracellular matrix glycoprotein that is expressed during inflammatory and fibrotic disorders, and specifically, is deposited in increased amounts in the asthmatic airway (Johnson PR. Clin Exp Pharmacol Physiol

30 2001 Mar;28(3):233-6). The preferential expression of this gene in cells derived from the

lung and skin suggests that this gene product may be involved in normal conditions as well as pathological and inflammatory lung and skin disorders that include chronic obstructive pulmonary disease, asthma, allergy, psoriasis and emphysema.

5   **AK. CG56054-02: Integrin alpha 7-like protein.**

Expression of gene CG56054-02 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6424, Ag6428, Ag6429, Ag6430, Ag6431, Ag6439, Ag6413 and Ag6964, described in Tables AKA, AKB, AKC, AKD, AKE, AKF, AKG, AKH, AKI and AKJ. Results of the RTQ-PCR runs are shown in Tables AKK, AKL, AKM, AKN, AKO and
10   AKP.

Table AKA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2435	414
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2457	415
Reverse	5'-aacagcagctctacctccagtt-3'	22	2491	416

Table AKB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2874	417
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2913	418
Reverse	5'-gcgcagtccagggtg-3'	15	2999	419

Table AKC. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	420

Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	761	421
Reverse	5'-aaaagcaaccccttccaa-3'	18	824	422

Table AKD. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1394	423
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1434	424
Reverse	5'-agggagtagccgaagctct-3'	19	1471	425

Table AKE. Probe Name Ag6429

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccgtgccccagtaccat-3'	17	3382	426
Probe	TET-5'-cgggcaccatcctgaggaacaac-3'-TAMRA	23	3448	427
Reverse	5'-gggcccagccaggat-3'	15	3484	428

Table AKF. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	843	429
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	866	430
Reverse	5'-gggagccggtcagca-3'	15	899	431

5   Table AKG. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2993	432
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	3034	433

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| Reverse | 5'-ccgcgcggtcaaa-3' | 13 | 3060 | 434 |

Table AKH. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	3250	435
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	3270	436
Reverse	5'-gaagaatcccatcttccacag-3'	21	3336	437

Table AKI. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	2073	438
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2124	439
Reverse	5'-gctgttgttccatccacatc-3'	20	2166	440

Table AKJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	3079	441
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	3050	442
Reverse	5'-gccaactgtgtggtgttca-3'	19	3024	443

5   Table AKK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6442, Run 264979298
AD 1 Hippo	23.7	24.8	18.0	20.0	18.8	21.6	19.2
AD 2 Hippo	41.2	52.9	32.3	48.0	28.7	28.9	49.7
AD 3 Hippo	8.9	6.4	3.7	11.6	7.5	6.1	20.4

AD 4 Hippo	14.8	25.5	10.7	17.1	18.8	17.6	5.6
AD 5 Hippo	44.8	41.8	53.2	39.2	38.4	42.6	57.4
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	100.0	90.1
Control 2 Hippo	24.3	36.1	18.7	17.9	29.5	32.5	28.5
Control 4 Hippo	42.9	43.8	27.0	38.4	32.3	37.9	86.5
Control (Path) 3 Hippo	14.2	11.4	4.6	10.2	6.0	6.4	0.0
AD 1 Temporal Ctx	23.3	15.9	12.9	12.1	17.1	24.5	16.8
AD 2 Temporal Ctx	41.5	47.3	31.0	36.6	39.8	27.5	21.6
AD 3 Temporal Ctx	9.5	9.8	6.0	11.7	11.3	9.0	5.7
AD 4 Temporal Ctx	30.6	39.0	20.2	15.6	25.3	30.4	8.7
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	43.8	36.3	41.8	73.7
AD 5 Sup Temporal Ctx	51.1	39.0	42.0	56.6	32.3	38.7	55.9
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	40.9	46.7	47.6	76.8
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	44.1	50.3	50.3	59.9
Control 1 Temporal Ctx	12.2	23.0	12.9	11.9	15.6	24.0	46.7
Control 2 Temporal Ctx	14.2	32.5	18.2	16.7	17.4	14.9	50.0

Control 3 Temporal Ctx	15.1	15.3	9.6	13.0	14.5	16.5	9.5
Control 3 Temporal Ctx	23.7	25.0	15.2	18.9	13.1	23.8	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	32.5	30.6	39.8	46.0
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	19.5	20.4	24.8	0.0
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	12.9	10.9	11.9	31.0
Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	19.8	18.2	21.6	39.5
AD 1 Occipital Ctx	16.0	11.9	10.2	16.2	11.5	16.0	6.3
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	11.7	8.8	10.2	4.9
AD 4 Occipital Ctx	18.9	23.7	13.0	12.6	17.9	18.6	11.1
AD 5 Occipital Ctx	24.8	28.3	25.3	16.7	22.5	22.7	42.3
AD 6 Occipital Ctx	20.6	31.9	20.2	17.8	17.0	22.1	14.8
Control 1 Occipital Ctx	9.5	14.4	6.0	11.3	8.7	7.2	8.8
Control 2 Occipital Ctx	31.9	42.6	26.4	24.8	33.2	29.3	82.4
Control 3 Occipital Ctx	18.8	13.0	10.7	16.4	17.1	19.2	8.8

Control 4 Occipital Ctx	18.2	17.0	12.0	12.1	12.6	13.6	24.0
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	32.8	36.1	39.5	**100.0**
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	9.6	7.9	7.0	9.3
Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	8.4	6.0	5.9	4.1
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	15.9	10.2	11.4	32.8
Control 1 Parietal Ctx	14.4	21.9	8.8	15.2	16.3	15.7	9.2
Control 2 Parietal Ctx	32.8	28.9	34.4	39.5	28.3	37.1	28.1
Control 3 Parietal Ctx	20.6	19.8	11.5	14.5	8.7	10.8	9.1
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	33.4	39.2	37.9	69.3
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	20.0	22.5	18.7	37.6
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	15.0	7.1	12.0	10.4
Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	28.3	8.8	27.9	27.5

Table AKL. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0

Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2

Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	100.0
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table AKM. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1

Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7

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Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

<u>Table AKN</u>. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	0.0	20.0	8.2	17.4	13.8	17.3	18.8
Melanoma* Hs688(A).T	0.5	0.0	2.0	0.5	0.8	0.9	0.4	0.7
Melanoma* Hs688(B).T	2.7	0.0	4.1	0.6	2.5	2.2	2.9	2.4
Melanoma* M14	0.3	0.0	0.7	0.7	0.4	0.4	0.4	0.7

Melanoma* LOXIMVI	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	15.2	0.0	30.4	22.5	18.2	14.6	18.3	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.3	0.1	0.2	0.0	0.1
Testis Pool	5.2	0.0	8.8	4.2	10.4	9.0	9.1	9.9
Prostate ca.* (bone met) PC-3	1.9	0.0	2.5	1.0	1.9	1.8	1.3	4.3
Prostate Pool	8.1	0.0	11.5	8.5	11.3	12.1	28.5	10.0
Placenta	0.5	0.0	0.7	0.1	0.1	0.1	0.5	0.4
Uterus Pool	2.2	0.0	4.5	2.6	4.6	4.5	5.3	4.1
Ovarian ca. OVCAR-3	0.9	0.0	1.1	0.8	0.7	1.1	1.6	4.0
Ovarian ca. SK-OV-3	0.8	0.0	1.7	1.5	0.8	0.9	1.3	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.9	0.5	0.4	0.8	0.9	0.5
Ovarian ca. OVCAR-5	1.6	0.0	2.9	1.5	1.3	1.7	1.4	7.9
Ovarian ca. IGROV-1	100.0	100.0	77.9	90.8	84.7	97.9	69.3	75.8
Ovarian ca. OVCAR-8	13.6	5.6	14.0	11.9	15.6	14.6	17.3	16.7
Ovary	2.7	0.0	5.2	2.1	3.1	2.3	2.8	2.4
Breast ca. MCF-7	0.3	0.0	0.3	0.4	0.1	0.2	0.5	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.4	0.4	0.2	0.2	0.2	0.3
Breast ca. BT 549	0.5	0.0	0.5	0.3	0.1	0.5	0.6	0.4
Breast ca. T47D	0.0	0.0	0.5	0.3	0.2	0.3	0.4	0.5

Breast ca. MDA-N	0.6	0.0	0.7	0.7	0.6	0.6	0.6	0.8
Breast Pool	15.0	0.0	21.8	19.5	14.6	10.7	12.2	16.7
Trachea	4.5	0.0	8.4	2.9	4.8	4.2	4.7	5.6
Lung	2.8	0.0	2.3	1.3	4.2	3.2	3.9	5.1
Fetal Lung	3.9	0.0	9.1	4.0	5.0	4.8	5.3	6.1
Lung ca. NCI-N417	2.0	2.0	3.5	2.7	3.3	2.6	4.0	2.3
Lung ca. LX-1	3.5	3.1	6.5	7.0	5.0	3.5	4.9	44.1
Lung ca. NCI-H146	0.1	0.0	0.3	0.5	0.1	0.2	0.1	0.1
Lung ca. SHP-77	4.0	2.3	6.8	6.3	5.3	4.5	4.5	3.8
Lung ca. A549	0.3	0.0	0.9	0.3	0.0	0.4	0.6	4.7
Lung ca. NCI-H526	0.2	0.0	0.9	0.7	0.6	0.3	0.4	0.5
Lung ca. NCI-H23	2.9	0.0	4.6	4.5	4.8	3.2	2.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.2	0.1	0.3	0.0	0.3
Lung ca. HOP-62	0.5	0.0	0.5	0.6	1.0	0.6	0.5	0.7
Lung ca. NCI-H522	1.7	0.0	2.3	2.4	1.7	1.3	3.3	8.9
Liver	0.1	0.0	0.0	0.1	0.0	0.0	0.1	2.0
Fetal Liver	0.3	0.0	1.1	0.6	0.6	0.5	0.8	8.2
Liver ca. HepG2	0.1	0.0	0.2	0.1	0.0	0.2	0.1	2.4
Kidney Pool	27.9	6.5	47.0	34.9	33.9	28.1	43.2	32.8
Fetal Kidney	1.4	0.0	4.9	5.1	4.1	4.0	5.8	11.5
Renal ca. 786-0	0.2	0.0	0.2	0.2	0.3	0.1	0.3	0.9

Renal ca. A498	0.0	0.0	0.2	0.1	0.0	0.3	0.5	8.5
Renal ca. ACHN	1.5	0.0	2.5	0.7	1.7	1.5	1.2	2.5
Renal ca. UO-31	0.3	0.0	0.5	0.3	0.2	0.2	0.6	0.3
Renal ca. TK-10	1.9	0.0	3.1	2.5	2.0	1.9	2.1	4.6
Bladder	4.2	0.0	5.9	3.0	5.5	5.1	8.3	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	1.7	1.7	0.9	1.2	1.1	6.7
Gastric ca. KATO III	0.4	0.0	0.8	0.4	0.2	0.3	0.4	0.9
Colon ca. SW-948	0.0	0.0	0.2	0.0	0.2	0.2	0.3	1.2
Colon ca. SW480	20.9	9.5	41.8	39.0	27.0	23.3	23.0	33.7
Colon ca.* (SW480 met) SW620	13.3	7.7	16.4	15.5	12.8	10.3	6.1	25.0
Colon ca. HT29	0.2	0.0	0.0	0.0	0.2	0.2	0.0	0.3
Colon ca. HCT-116	2.1	1.6	3.2	3.8	2.5	2.0	2.1	4.3
Colon ca. CaCo-2	15.0	10.4	27.0	22.2	19.1	16.7	18.3	38.2
Colon cancer tissue	9.0	0.0	11.0	6.5	11.9	7.6	7.7	20.4
Colon ca. SW1116	1.3	0.0	2.5	1.7	2.0	1.5	1.8	6.0
Colon ca. Colo-205	0.1	0.0	0.3	0.2	0.2	0.0	0.2	0.8
Colon ca. SW-48	0.8	0.0	1.4	1.3	1.5	1.5	1.4	2.6
Colon Pool	20.3	0.0	28.1	28.7	23.2	18.7	25.5	20.6

Small Intestine Pool	14.0	0.0	17.1	10.5	11.2	13.0	12.8	10.4
Stomach Pool	8.1	0.0	14.3	6.2	9.5	9.3	8.5	10.7
Bone Marrow Pool	6.8	0.0	14.3	11.3	10.2	8.7	18.7	12.5
Fetal Heart	10.1	0.0	25.5	24.3	24.5	21.8	33.7	20.7
Heart Pool	28.7	5.2	29.7	23.0	25.9	17.2	33.7	26.1
Lymph Node Pool	17.6	0.0	33.7	30.4	22.1	23.7	19.9	24.7
Fetal Skeletal Muscle	31.9	36.9	54.3	46.7	48.6	46.3	19.1	50.7
Skeletal Muscle Pool	17.4	12.3	29.3	21.5	29.5	25.9	22.1	32.3
Spleen Pool	0.9	0.0	1.9	2.0	2.0	1.7	2.7	3.1
Thymus Pool	4.4	0.0	10.4	7.5	8.1	9.4	7.7	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.6	14.9	6.1	10.7	10.0	10.9	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.0	4.7	2.9	3.8	3.1	3.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	2.6	1.7	2.1	1.0	1.4	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.2	0.1	0.2	0.1	0.1
CNS cancer (astro) SNB-75	8.1	1.9	14.9	5.9	6.5	10.0	11.7	9.7
CNS cancer (glio) SNB-19	79.6	84.1	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**
CNS cancer (glio) SF-295	8.2	1.8	11.3	9.0	8.0	7.8	8.2	14.8

Brain (Amygdala) Pool	3.7	2.3	7.7	6.9	6.2	4.8	8.0	5.3
Brain (cerebellum)	12.0	6.6	19.8	11.1	10.7	9.7	8.8	9.7
Brain (fetal)	4.2	3.0	12.7	11.5	6.6	5.6	6.8	6.4
Brain (Hippocampus) Pool	7.5	3.1	11.7	11.0	8.6	6.9	11.0	10.2
Cerebral Cortex Pool	9.7	1.7	11.0	7.5	7.5	0.7	11.6	8.7
Brain (Substantia nigra) Pool	7.4	1.8	11.7	8.5	10.4	4.7	10.0	9.3
Brain (Thalamus) Pool	7.6	0.0	13.2	10.0	9.3	0.2	9.7	8.7
Brain (whole)	6.1	0.0	10.6	8.0	5.8	0.3	5.6	8.7
Spinal Cord Pool	10.1	3.2	14.7	12.8	11.0	7.6	12.2	9.0
Adrenal Gland	3.5	0.0	9.9	6.1	3.9	3.7	4.8	4.1
Pituitary gland Pool	0.9	0.0	1.1	0.8	1.2	1.1	1.4	0.5
Salivary Gland	0.9	0.0	1.8	1.1	1.3	0.9	1.1	1.0
Thyroid (female)	2.0	0.0	3.1	0.8	2.5	2.5	1.9	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.8	0.8	0.7	0.6	0.7	2.2
Pancreas Pool	1.2	0.0	2.0	1.1	1.1	1.6	3.2	2.3

Table AKO. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.1	0.3	1.3	0.0	0.7	0.0
Secondary Th2 act	0.5	0.3	1.2	0.0	0.8	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.7	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.4	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.3	0.0	0.4	0.0
Primary Tr1 act	0.1	0.0	0.7	0.0	0.7	0.0
Primary Th1 rest	0.0	0.0	0.1	0.0	0.3	1.2
Primary Th2 rest	0.0	0.0	0.4	0.0	0.2	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	5.4	0.0	2.4	2.6
CD45RO CD4 lymphocyte act	0.1	2.2	1.5	0.0	0.7	2.3
CD8 lymphocyte act	0.4	0.9	0.7	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	8.8	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.4	0.0	0.3	0.0
CD4 lymphocyte none	0.1	0.0	0.5	0.0	0.4	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	1.2
LAK cells rest	5.6	5.0	11.8	0.1	3.8	15.2
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0

LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.1	0.1	6.3	9.0
NK Cells IL-2 rest	0.9	0.1	3.4	0.0	2.5	1.4
Two Way MLR 3 day	1.4	1.1	2.2	0.0	1.3	1.4
Two Way MLR 5 day	4.5	0.9	0.8	0.0	0.9	0.0
Two Way MLR 7 day	2.3	0.7	1.1	0.0	2.6	3.7
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	1.3	0.0	0.0	0.0
PBMC PHA-L	0.3	0.2	0.6	0.0	0.7	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.7	0.0	0.2	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.9	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	29.1	0.1	8.1	68.8
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	2.7	1.8
Dendritic cells none	5.6	3.1	4.1	0.0	5.3	0.0
Dendritic cells LPS	1.6	0.3	1.0	0.0	0.7	0.0
Dendritic cells anti-CD40	2.0	1.6	0.5	0.0	0.2	0.0
Monocytes rest	0.2	0.0	0.4	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	5.7	0.0	1.8	2.6
Macrophages rest	0.9	1.8	0.6	0.0	0.6	0.0
Macrophages LPS	7.5	4.0	5.4	0.1	6.3	9.2
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.3	0.0

HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.5	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.4	0.0
HUVEC IL-11	0.0	0.0	0.4	0.0	0.3	0.0
Lung Microvascular EC none	0.2	0.3	0.4	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	0.3	0.0	1.5	0.0
Astrocytes rest	67.8	97.3	**100.0**	12.0	**100.0**	**100.0**
Astrocytes TNFalpha + IL-1beta	**100.0**	**100.0**	97.3	**100.0**	74.7	95.9
KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.4	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0

CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.8	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	2.6	0.0	6.7	8.5
NCI-H292 none	0.3	0.3	1.7	0.0	0.6	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.5	0.0
NCI-H292 IL-9	0.3	0.0	0.7	0.0	0.5	0.0
NCI-H292 IL-13	0.6	0.6	0.9	0.0	0.9	0.0
NCI-H292 IFN gamma	0.2	0.0	0.5	0.0	0.6	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	95.9	0.2	65.5	94.0
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	48.6	0.1	39.8	62.9
Lung fibroblast IL-4	26.1	28.7	27.4	0.1	21.2	34.9
Lung fibroblast IL-9	28.5	42.0	24.0	0.1	26.8	96.6
Lung fibroblast IL-13	31.6	14.6	11.9	0.0	10.4	13.4
Lung fibroblast IFN gamma	20.4	32.8	55.9	0.2	46.3	89.5
Dermal fibroblast CCD1070 rest	2.5	2.9	6.0	0.0	6.3	4.1
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	2.7	0.0	0.8	2.3
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	5.6	0.0	1.3	0.0
Dermal fibroblast IFN gamma	9.3	20.3	30.6	0.1	20.2	26.6
Dermal fibroblast IL-4	10.7	14.6	30.8	0.1	19.8	25.5
Dermal Fibroblasts rest	24.8	42.3	54.3	0.1	46.7	47.3

Neutrophils TNFa+LPS	0.7	0.0	0.9	0.0	0.4	0.0
Neutrophils rest	0.1	0.0	0.0	0.0	0.3	0.0
Colon	7.9	4.7	4.6	0.0	9.5	8.4
Lung	2.2	1.2	2.8	0.0	4.6	2.1
Thymus	3.1	0.8	0.0	0.0	0.4	2.4
Kidney	4.2	4.4	7.8	0.1	9.7	5.2

Table AKP. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2

Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0

Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus,

cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

5   General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the 10   regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6

15   Summary: Ag6413/Ag6424/Ag6428/Ag6430/Ag6431/Ag6439/Ag6964 Eight experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous 20   system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6429 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D

25   Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

30   In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by

colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus

5   erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

Ag6424 Expression of this gene is low/undetectable (CTs > 35) across all of the

10   samples on this panel (data not shown).

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore,

15   expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to

20   detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AL. CG56054-03: Integrin alpha 7-like protein.

Expression of gene CG56054-03 was assessed using the primer-probe sets Ag6424,

25   Ag6425, Ag6428, Ag6430 and Ag6432, described in Tables ALA, ALB, ALC, ALD and ALE. Results of the RTQ-PCR runs are shown in Tables ALF, ALG and ALH.

Table ALA. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	444

Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	761	445
Reverse	5'-aaaagcaaccccttccaa-3'	18	824	446

Table ALB. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacacccat-3'	16	1981	447
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	2013	448
Reverse	5'-gccctggatgcccat-3'	15	2032	449

Table ALC. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1394	450
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1434	451
Reverse	5'-agggagtagccgaagctct-3'	19	1471	452

Table ALD. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	843	453
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	866	454
Reverse	5'-gggagccggtcagca-3'	15	899	455

Table ALE. Probe Name Ag6432

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gaccttgtcctacagtctccagac-3'	24	1934	456

| Probe | TET-5'-.tgcacaccccatcctggctgct-3'-TAMRA | 22 | 1985 | 457 |
| Reverse | 5'-gctcgggatgcccgt-3' | 15 | 2008 | 458 |

Table ALF. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085
AD 1 Hippo	18.0	20.0
AD 2 Hippo	32.3	48.0
AD 3 Hippo	3.7	11.6
AD 4 Hippo	10.7	17.1
AD 5 hippo	53.2	39.2
AD 6 Hippo	**100.0**	**100.0**
Control 2 Hippo	18.7	17.9
Control 4 Hippo	27.0	38.4
Control (Path) 3 Hippo	4.6	10.2
AD 1 Temporal Ctx	12.9	12.1
AD 2 Temporal Ctx	31.0	36.6
AD 3 Temporal Ctx	6.0	11.7
AD 4 Temporal Ctx	20.2	15.6
AD 5 Inf Temporal Ctx	39.2	43.8
AD 5 SupTemporal Ctx	42.0	56.6
AD 6 Inf Temporal Ctx	49.3	40.9
AD 6 Sup Temporal Ctx	48.3	44.1
Control 1 Temporal Ctx	12.9	11.9
Control 2 Temporal Ctx	18.2	16.7
Control 3 Temporal Ctx	9.6	13.0
Control 4 Temporal Ctx	15.2	18.9
Control (Path) 1 Temporal Ctx	27.0	32.5
Control (Path) 2 Temporal Ctx	16.0	19.5

Control (Path) 3 Temporal Ctx	7.5	12.9
Control (Path) 4 Temporal Ctx	17.1	19.8
AD 1 Occipital Ctx	10.2	16.2
AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 3 Occipital Ctx	6.4	11.7
AD 4 Occipital Ctx	13.0	12.6
AD 5 Occipital Ctx	25.3	16.7
AD 6 Occipital Ctx	20.2	17.8
Control 1 Occipital Ctx	6.0	11.3
Control 2 Occipital Ctx	26.4	24.8
Control 3 Occipital Ctx	10.7	16.4
Control 4 Occipital Ctx	12.0	12.1
Control (Path) 1 Occipital Ctx	35.6	32.8
Control (Path) 2 Occipital Ctx	6.7	9.6
Control (Path) 3 Occipital Ctx	5.4	8.4
Control (Path) 4 Occipital Ctx	13.2	15.9
Control 1 Parietal Ctx	8.8	15.2
Control 2 Parietal Ctx	34.4	39.5
Control 3 Parietal Ctx	11.5	14.5
Control (Path) 1 Parietal Ctx	34.2	33.4
Control (Path) 2 Parietal Ctx	19.6	20.0
Control (Path) 3 Parietal Ctx	3.9	15.0
Control (Path) 4 Parietal Ctx	24.8	28.3

Table ALG. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443
Adipose	0.0	2.6	20.0	8.2

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Melanoma* Hs688(A).T	0.0	0.0	2.0	0.5
Melanoma* Hs688(B).T	0.0	0.2	4.1	0.6
Melanoma* M14	0.0	0.0	0.7	0.7
Melanoma* LOXIMVI	0.0	0.0	0.1	0.0
Melanoma* SK-MEL-5	0.0	2.2	30.4	22.5
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.3
Testis Pool	0.0	3.5	8.8	4.2
Prostate ca.* (bone met) PC-3	0.0	0.5	2.5	1.0
Prostate Pool	0.0	1.0	11.5	8.5
Placenta	0.0	0.0	0.7	0.1
Uterus Pool	0.0	1.5	4.5	2.6
Ovarian ca. OVCAR-3	0.0	0.3	1.1	0.8
Ovarian ca. SK-OV-3	0.0	0.2	1.7	1.5
Ovarian ca. OVCAR-4	0.0	0.0	0.9	0.5
Ovarian ca. OVCAR-5	0.0	1.3	2.9	1.5
Ovarian ca. IGROV-1	100.0	100.0	77.9	90.8
Ovarian ca. OVCAR-8	5.6	21.9	14.0	11.9
Ovary	0.0	0.3	5.2	2.1
Breast ca. MCF-7	0.0	0.0	0.3	0.4
Breast ca. MDA-MB-231	0.0	0.0	0.4	0.4
Breast ca. BT 549	0.0	0.0	0.5	0.3
Breast ca. T47D	0.0	0.0	0.5	0.3
Breast ca. MDA-N	0.0	0.0	0.7	0.7
Breast Pool	0.0	4.1	21.8	19.5
Trachea	0.0	0.7	8.4	2.9
Lung	0.0	0.7	2.3	1.3
Fetal Lung	0.0	0.3	9.1	4.0
Lung ca. NCI-N417	2.0	0.9	3.5	2.7

Lung ca. LX-1	3.1	2.7	6.5	7.0
Lung ca. NCI-H146	0.0	0.0	0.3	0.5
Lung ca. SHP-77	2.3	0.4	6.8	6.3
Lung ca. A549	0.0	2.6	0.9	0.3
Lung ca. NCI-H526	0.0	0.0	0.9	0.7
Lung ca. NCI-H23	0.0	1.0	4.6	4.5
Lung ca. NCI-H460	0.0	0.0	0.2	0.2
Lung ca. HOP-62	0.0	0.0	0.5	0.6
Lung ca. NCI-H522	0.0	0.6	2.3	2.4
Liver	0.0	0.0	0.0	0.1
Fetal Liver	0.0	0.3	1.1	0.6
Liver ca. HepG2	0.0	0.3	0.2	0.1
Kidney Pool	6.5	0.0	47.0	34.9
Fetal Kidney	0.0	0.0	4.9	5.1
Renal ca. 786-0	0.0	0.0	0.2	0.2
Renal ca. A498	0.0	1.8	0.2	0.1
Renal ca. ACHN	0.0	0.5	2.5	0.7
Renal ca. UO-31	0.0	0.0	0.5	0.3
Renal ca. TK-10	0.0	0.4	3.1	2.5
Bladder	0.0	0.0	5.9	3.0
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.7	1.7
Gastric ca. KATO III	0.0	0.5	0.8	0.4
Colon ca. SW-948	0.0	1.5	0.2	0.0
Colon ca. SW480	9.5	5.2	41.8	39.0
Colon ca.* (SW480 met) SW620	7.7	4.8	16.4	15.5
Colon ca. HT29	0.0	0.0	0.0	0.0
Colon ca. HCT-116	1.6	0.2	3.2	3.8
Colon ca. CaCo-2	10.4	3.6	27.0	22.2
Colon cancer tissue	0.0	3.3	11.0	6.5
Colon ca. SW1116	0.0	3.0	2.5	1.7

Colon ca. Colo-205	0.0	0.4	0.3	0.2
Colon ca. SW-48	0.0	3.6	1.4	1.3
Colon Pool	0.0	5.0	28.1	28.7
Small Intestine Pool	0.0	1.7	17.1	10.5
Stomach Pool	0.0	2.3	14.3	6.2
Bone Marrow Pool	0.0	1.6	14.3	11.3
Fetal Heart	0.0	2.3	25.5	24.3
Heart Pool	5.2	7.0	29.7	23.0
Lymph Node Pool	0.0	6.1	33.7	30.4
Fetal Skeletal Muscle	36.9	5.2	54.3	46.7
Skeletal Muscle Pool	12.3	9.2	29.3	21.5
Spleen Pool	0.0	0.0	1.9	2.0
Thymus Pool	0.0	2.0	10.4	7.5
CNS cancer (glio/astro) U87-MG	1.6	1.5	14.9	6.1
CNS cancer (glio/astro) U-118-MG	0.0	0.3	4.7	2.9
CNS cancer (neuro;met) SK-N-AS	0.0	0.0	2.6	1.7
CNS cancer (astro) SF-539	0.0	0.0	0.0	0.2
CNS cancer (astro) SNB-75	1.9	1.1	14.9	5.9
CNS cancer (glio) SNB-19	84.1	79.0	**100.0**	**100.0**
CNS cancer (glio) SF-295	1.8	0.0	11.3	9.0
Brain (Amygdala) Pool	2.3	0.8	7.7	6.9
Brain (cerebellum)	6.6	0.4	19.8	11.1
Brain (fetal)	3.0	0.7	12.7	11.5
Brain (Hippocampus) Pool	3.1	3.2	11.7	11.0
Cerebral Cortex Pool	1.7	0.6	11.0	7.5
Brain (Substantia nigra) Pool	1.8	2.2	11.7	8.5

Brain (Thalamus) Pool	0.0	2.7	13.2	10.0
Brain (whole)	0.0	0.4	10.6	8.0
Spinal Cord Pool	3.2	2.3	14.7	12.8
Adrenal Gland	0.0	0.3	9.9	6.1
Pituitary gland Pool	0.0	0.0	1.1	0.8
Salivary Gland	0.0	0.0	1.8	1.1
Thyroid (female)	0.0	0.3	3.1	0.8
Pancreatic ca. CAPAN2	0.0	0.0	0.8	0.8
Pancreas Pool	0.0	0.0	2.0	1.1

Table ALH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6430, Run 268767563
Secondary Th1 act	0.0	1.3	0.0
Secondary Th2 act	0.0	1.2	0.0
Secondary Tr1 act	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.4	0.0
Primary Th1 act	0.0	0.0	0.0
Primary Th2 act	0.0	0.3	0.0
Primary Tr1 act	0.0	0.7	0.0
Primary Th1 rest	0.0	0.1	0.0
Primary Th2 rest	0.0	0.4	0.0
Primary Tr1 rest	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	5.4	0.0
CD45RO CD4 lymphocyte act	0.0	1.5	0.0
CD8 lymphocyte act	0.0	0.7	0.0
Secondary CD8 lymphocyte rest	0.0	8.8	0.0
Secondary CD8 lymphocyte act	0.0	0.4	0.0

CD4 lymphocyte none	0.0	0.5	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	0.0
LAK cells rest	2.7	11.8	0.1
LAK cells IL-2	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	15.1	0.1
NK Cells IL-2 rest	0.0	3.4	0.0
Two Way MLR 3 day	0.0	2.2	0.0
Two Way MLR 5 day	0.0	0.8	0.0
Two Way MLR 7 day	13.2	1.1	0.0
PBMC rest	0.0	0.0	0.0
PBMC PWM	0.0	1.3	0.0
PBMC PHA-L	0.0	0.6	0.0
Ramos (B cell) none	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.7	0.0
B lymphocytes PWM	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.9	0.0
EOL-1 dbcAMP	9.1	29.1	0.1
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	0.0
Dendritic cells none	13.8	4.1	0.0
Dendritic cells LPS	0.0	1.0	0.0
Dendritic cells anti-CD40	3.3	0.5	0.0
Monocytes rest	0.0	0.4	0.0
Monocytes LPS	0.0	5.7	0.0
Macrophages rest	0.0	0.6	0.0
Macrophages LPS	0.0	5.4	0.1
HUVEC none	0.0	0.0	0.0

HUVEC starved	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.4	0.0
Lung Microvascular EC none	0.0	0.4	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.3	0.0
Astrocytes rest	100.0	100.0	12.0
Astrocytes TNFalpha + IL-1beta	74.2	97.3	100.0
KU-812 (Basophil) rest	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0
Liver cirrhosis	4.6	2.6	0.0
NCI-H292 none	0.0	1.7	0.0
NCI-H292 IL-4	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.7	0.0

NCI-H292 IL-13	0.0	0.9	0.0
NCI-H292 IFN gamma	0.0	0.5	0.0
HPAEC none	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0
Lung fibroblast none	31.4	95.9	0.2
Lung fibroblast TNF alpha + IL-1 beta	22.2	48.6	0.1
Lung fibroblast IL-4	19.1	27.4	0.1
Lung fibroblast IL-9	23.5	24.0	0.1
Lung fibroblast IL-13	4.5	11.9	0.0
Lung fibroblast IFN gamma	15.7	55.9	0.2
Dermal fibroblast CCD1070 rest	0.0	6.0	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	2.7	0.0
Dermal fibroblast CCD1070 IL-1 beta	0.0	5.6	0.0
Dermal fibroblast IFN gamma	8.5	30.6	0.1
Dermal fibroblast IL-4	4.1	30.8	0.1
Dermal Fibroblasts rest	8.0	54.3	0.1
Neutrophils TNFa+LPS	0.0	0.9	0.0
Neutrophils rest	0.0	0.0	0.0
Colon	4.0	4.6	0.0
Lung	0.0	2.8	0.0
Thymus	0.0	0.0	0.0
Kidney	4.9	7.8	0.1

CNS_neurodegeneration_v1.0 Summary: Ag6428/Ag6430 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6 Summary: Ag6424/Ag6425/Ag6428/Ag6430
Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain
cancer SNB-19 cell lines (CTs=25-31). In addition, consistent with expression seen in panel
1.4, moderate to low levels of expression of this gene is also seen in all the regions of

5   central nervous system, tissues with metabolic/endocrine functions, and number of cancer
cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D Summary Ag6425/Ag6428/Ag6430 Highest expression of this gene is
detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore,
therapeutic modulation of this gene or the design of therapeutics with the encoded protein

10   could be important in the treatment of multiple sclerosis or other inflammatory diseases of
the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting
and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by
colon, lung, thymus and kidney. Therefore, modulation of the gene product with a

15   functional therapeutic may lead to the alteration of functions associated with these cell types
and lead to improvement of the symptoms of patients suffering from autoimmune and
inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus
erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Ag6424/Ag6432 Expression of this gene is low/undetectable (CTs > 35) across all

20   of the samples on this panel (data not shown).

AM. CG56054-04: Integrin alpha 7-like protein.

Expression of gene CG56054-04 was assessed using the primer-probe sets Ag6424,
Ag6427, Ag6430 and Ag6434, described in Tables AMA, AMB, AMC and AMD. Results
of the RTQ-PCR runs are shown in Tables AME, AMF and AMG.

25   <u>Table AMA</u>. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	459
Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	761	460
Reverse	5'-aaaagcaaccccttccaa-3'	18	824	461

Table AMB. Probe Name Ag6427

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1394	462
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1434	463
Reverse	5'-ccctggatgcccatc-3'	15	1484	464

Table AMC. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	843	465
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	866	466
Reverse	5'-gggagccggtcagca-3'	15	899	467

Table AMD. Probe Name Ag6434

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctttgatggtgatgggaa-3'	19	1372	468
Probe	TET-5'-cttcatctaccatgggagcagcctg-3'-TAMRA	25	1394	469
Reverse	5'-gctcgggatgcccac-3'	15	1461	470

5   Table AME. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6434, Run 269253996	Tissue Name	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6434, Run 269253996
AD 1 Hippo	20.0	17.3	Control (Path) 3 Temporal Ctx	12.9	9.2
AD 2 Hippo	48.0	33.0	Control (Path) 4 Temporal Ctx	19.8	13.8
AD 3 Hippo	11.6	3.4	AD 1 Occipital Ctx	16.2	8.4

AD 4 Hippo	17.1	9.0	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	39.2	66.4	AD 3 Occipital Ctx	11.7	3.8
AD 6 Hippo	**100.0**	**100.0**	AD 4 Occipital Ctx	12.6	1.4
Control 2 Hippo	17.9	23.3	AD 5 Occipital Ctx	16.7	21.3
Control 4 Hippo	38.4	26.6	AD 6 Occipital Ctx	17.8	15.5
Control (Path) 3 Hippo	10.2	7.0	Control 1 Occipital Ctx	11.3	5.5
AD 1 Temporal Ctx	12.1	13.7	Control 2 Occipital Ctx	24.8	33.7
AD 2 Temporal Ctx	36.6	35.8	Control 3 Occipital Ctx	16.4	3.0
AD 3 Temporal Ctx	11.7	7.2	Control 4 Occipital Ctx	12.1	8.1
AD 4 Temporal Ctx	15.6	6.7	Control (Path) 1 Occipital Ctx	32.8	39.0
AD 5 Inf Temporal Ctx	43.8	21.9	Control (Path) 2 Occipital Ctx	9.6	4.2
AD 5 SupTemporal Ctx	56.6	31.6	Control (Path) 3 Occipital Ctx	8.4	3.2
AD 6 Inf Temporal Ctx	40.9	52.9	Control (Path) 4 Occipital Ctx	15.9	9.3
AD 6 Sup Temporal Ctx	44.1	71.2	Control 1 Parietal Ctx	15.2	10.1
Control 1 Temporal Ctx	11.9	10.3	Control 2 Parietal Ctx	39.5	43.5
Control 2 Temporal Ctx	16.7	16.2	Control 3 Parietal Ctx	14.5	15.9
Control 3 Temporal Ctx	13.0	8.5	Control (Path) 1 Parietal Ctx	33.4	24.8
Control 4 Temporal Ctx	18.9	13.6	Control (Path) 2 Parietal Ctx	20.0	22.1
Control (Path) 1 Temporal Ctx	32.5	29.9	Control (Path) 3 Parietal Ctx	15.0	9.3

Control (Path) 2 Temporal Ctx	19.5	13.2	Control (Path) 4 Parietal Ctx	28.3	34.6

Table AMF. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6427, Run 277222437	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6434, Run 277222451
Adipose	0.0	0.0	8.2	9.5
Melanoma* Hs688(A).T	0.0	0.0	0.5	0.9
Melanoma* Hs688(B).T	0.0	0.0	0.6	3.7
Melanoma* M14	0.0	0.0	0.7	0.7
Melanoma* LOXIMVI	0.0	0.0	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	22.5	14.7
Squamous cell carcinoma SCC-4	0.0	0.0	0.3	0.0
Testis Pool	0.0	0.0	4.2	5.7
Prostate ca.* (bone met) PC-3	0.0	0.0	1.0	1.5
Prostate Pool	0.0	0.0	8.5	4.2
Placenta	0.0	0.0	0.1	0.5
Uterus Pool	0.0	0.0	2.6	2.5
Ovarian ca. OVCAR-3	0.0	0.0	0.8	0.8
Ovarian ca. SK-OV-3	0.0	0.0	1.5	0.8
Ovarian ca. OVCAR-4	0.0	0.0	0.5	0.5
Ovarian ca. OVCAR-5	0.0	0.0	1.5	2.9
Ovarian ca. IGROV-1	100.0	100.0	90.8	73.7
Ovarian ca. OVCAR-8	5.6	0.0	11.9	20.7
Ovary	0.0	0.0	2.1	4.0
Breast ca. MCF-7	0.0	0.0	0.4	0.5
Breast ca. MDA-MB-231	0.0	0.0	0.4	0.5
Breast ca. BT 549	0.0	0.0	0.3	0.5
Breast ca. T47D	0.0	0.0	0.3	0.0

Breast ca. MDA-N	0.0	0.0	0.7	0.0
Breast Pool	0.0	0.0	19.5	9.6
Trachea	0.0	0.0	2.9	5.3
Lung	0.0	0.0	1.3	1.3
Fetal Lung	0.0	0.0	4.0	5.0
Lung ca. NCI-N417	2.0	0.0	2.7	3.0
Lung ca. LX-1	3.1	0.0	7.0	4.3
Lung ca. NCI-H146	0.0	0.0	0.5	0.0
Lung ca. SHP-77	2.3	0.0	6.3	4.9
Lung ca. A549	0.0	0.0	0.3	0.7
Lung ca. NCI-H526	0.0	0.0	0.7	0.0
Lung ca. NCI-H23	0.0	0.0	4.5	3.1
Lung ca. NCI-H460	0.0	0.0	0.2	0.0
Lung ca. HOP-62	0.0	0.0	0.6	0.0
Lung ca. NCI-H522	0.0	0.0	2.4	1.4
Liver	0.0	0.0	0.1	0.0
Fetal Liver	0.0	0.0	0.6	0.5
Liver ca. HepG2	0.0	0.0	0.1	0.5
Kidney Pool	6.5	0.0	34.9	22.8
Fetal Kidney	0.0	0.0	5.1	2.4
Renal ca. 786-0	0.0	0.0	0.2	0.0
Renal ca. A498	0.0	0.0	0.1	0.0
Renal ca. ACHN	0.0	0.0	0.7	0.7
Renal ca. UO-31	0.0	0.0	0.3	0.0
Renal ca. TK-10	0.0	0.0	2.5	3.0
Bladder	0.0	0.0	3.0	3.4
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.7	1.1
Gastric ca. KATO III	0.0	0.0	0.4	0.0
Colon ca. SW-948	0.0	0.0	0.0	0.0
Colon ca. SW480	9.5	0.0	39.0	28.3

Colon ca.* (SW480 met) SW620	7.7	0.0	15.5	11.7
Colon ca. HT29	0.0	0.0	0.0	0.0
Colon ca. HCT-116	1.6	0.0	3.8	5.0
Colon ca. CaCo-2	10.4	0.0	22.2	14.9
Colon cancer tissue	0.0	0.0	6.5	9.2
Colon ca. SW1116	0.0	0.0	1.7	2.2
Colon ca. Colo-205	0.0	0.0	0.2	0.0
Colon ca. SW-48	0.0	0.0	1.3	1.4
Colon Pool	0.0	0.0	28.7	14.2
Small Intestine Pool	0.0	0.0	10.5	7.4
Stomach Pool	0.0	0.0	6.2	9.2
Bone Marrow Pool	0.0	0.0	11.3	4.6
Fetal Heart	0.0	0.0	24.3	11.3
Heart Pool	5.2	0.0	23.0	15.2
Lymph Node Pool	0.0	0.0	30.4	14.1
Fetal Skeletal Muscle	36.9	0.0	46.7	33.0
Skeletal Muscle Pool	12.3	0.0	21.5	21.2
Spleen Pool	0.0	0.0	2.0	1.2
Thymus Pool	0.0	0.0	7.5	6.1
CNS cancer (glio/astro) U87-MG	1.6	0.0	6.1	10.4
CNS cancer (glio/astro) U-118-MG	0.0	0.0	2.9	3.4
CNS cancer (neuro;met) SK-N-AS	0.0	0.0	1.7	1.8
CNS cancer (astro) SF-539	0.0	0.0	0.2	0.0
CNS cancer (astro) SNB-75	1.9	0.0	5.9	12.0
CNS cancer (glio) SNB-19	84.1	25.0	100.0	100.0
CNS cancer (glio) SF-295	1.8	0.0	9.0	7.7

Brain (Amygdala) Pool	2.3	0.0	6.9	5.5
Brain (cerebellum)	6.6	0.0	11.1	11.0
Brain (fetal)	3.0	0.0	11.5	6.9
Brain (Hippocampus) Pool	3.1	0.0	11.0	8.5
Cerebral Cortex Pool	1.7	0.0	7.5	6.8
Brain (Substantia nigra) Pool	1.8	0.0	8.5	5.2
Brain (Thalamus) Pool	0.0	0.0	10.0	6.8
Brain (whole)	0.0	0.0	8.0	6.8
Spinal Cord Pool	3.2	0.0	12.8	6.4
Adrenal Gland	0.0	0.0	6.1	8.4
Pituitary gland Pool	0.0	0.0	0.8	0.6
Salivary Gland	0.0	0.0	1.1	1.6
Thyroid (female)	0.0	0.0	0.8	2.6
Pancreatic ca. CAPAN2	0.0	0.0	0.8	0.9
Pancreas Pool	0.0	0.0	1.1	0.8

Table AMG. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6434, Run 268713326	Tissue Name	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6434, Run 268713326
Secondary Th1 act	0.0	0.0	HUVEC IL-1beta	0.0	0.0
Secondary Th2 act	0.0	0.0	HUVEC IFN gamma	0.0	0.0
Secondary Tr1 act	0.0	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	0.0	0.0	HUVEC IL-11	0.0	0.0
Secondary Tr1 rest	0.0	0.0	Lung Microvascular EC none	0.0	0.0
Primary Th1 act	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0

Primary Th2 act	0.0	0.0	Microvascular Dermal EC none	0.0	0.0
Primary Tr1 act	0.0	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0
Primary Th2 rest	0.0	0.0	Small airway epithelium none	0.0	0.0
Primary Tr1 rest	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.0	Coronery artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	3.9	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	0.0	0.0	Astrocytes rest	12.0	**100.0**
Secondary CD8 lymphocyte rest	0.0	0.0	Astrocytes TNFalpha + IL-1beta	**100.0**	97.3
Secondary CD8 lymphocyte act	0.0	0.0	KU-812 (Basophil) rest	0.0	0.0
CD4 lymphocyte none	0.0	0.0	KU-812 (Basophil) PMA/ionomycin	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	CCD1106 (Keratinocytes) none	0.0	0.0
LAK cells rest	0.1	7.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	0.0	0.0	Liver cirrhosis	0.0	3.4
LAK cells IL-2+IL-12	0.0	0.0	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	NCI-H292 IL-4	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	0.1	7.0	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	0.0	0.0	NCI-H292 IFN gamma	0.0	0.0

Two Way MLR 3 day	0.0	0.0	HPAEC none	0.0	0.0
Two Way MLR 5 day	0.0	0.0	HPAEC TNF alpha + IL-1 beta	0.0	0.0
Two Way MLR 7 day	0.0	0.0	Lung fibroblast none	0.2	72.7
PBMC rest	0.0	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.1	36.6
PBMC PWM	0.0	0.0	Lung fibroblast IL-4	0.1	62.4
PBMC PHA-L	0.0	0.0	Lung fibroblast IL-9	0.1	52.5
Ramos (B cell) none	0.0	0.0	Lung fibroblast IL-13	0.0	14.6
Ramos (B cell) ionomycin	0.0	0.0	Lung fibroblast IFN gamma	0.2	41.5
B lymphocytes PWM	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	5.1
B lymphocytes CD40L and IL-4	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0	7.2
EOL-1 dbcAMP	0.1	4.4	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	Dermal fibroblast IFN gamma	0.1	24.5
Dendritic cells none	0.0	4.5	Dermal fibroblast IL-4	0.1	28.7
Dendritic cells LPS	0.0	0.0	Dermal Fibroblasts rest	0.1	44.4
Dendritic cells anti-CD40	0.0	0.0	Neutrophils TNFa+LPS	0.0	0.0
Monocytes rest	0.0	0.0	Neutrophils rest	0.0	0.0
Monocytes LPS	0.0	5.9	Colon	0.0	4.1
Macrophages rest	0.0	0.0	Lung	0.0	0.0
Macrophages LPS	0.1	9.1	Thymus	0.0	0.0
HUVEC none	0.0	0.0	Kidney	0.1	8.1
HUVEC starved	0.0	0.0			

CNS_neurodegeneration_v1.0 Summary: Ag6430/Ag6434 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this

experiment. See Panel 1.6 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6 Summary: Ag6424/Ag6430/Ag6434 Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer

5   SNB-19 cell lines (CTs=25-33.7). In addition, moderate to low levels of expression of this gene is also seen in some of the colon, ovarian and brain cancer cell lines. Thus, expression of this gene may be used as a marker to detect the presence of colon, ovarian and brain cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of these cancers. Moderate to low levels of expression of this gene is also seen in all the

10   regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. Moderate levels of expression of this gene is seen in normal tissues represented by breast, testis, prostate, uterus, gastrointestinal tract, and tissues with metabolic/endocrine functions including adipose, heart, skeletal muscle, and adernal gland. Therefore, therapeutic modulation of this gene or its protein product may be useful in the

15   treatment of diseases associated with these tissues, including obesity, diabetes and inflammatory bowel disease. In addition, moderate to low levels of expression of this gene is also seen in some regions of central nervous system, and some brain, colon and ovarian cancer cell lines.

Panel 4.1D Summary: Ag6430/Ag6434 Highest expression of this gene is detected

20   in both resting and cytokine activated astrocytes (CTs=22-34.8). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by

25   colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

30   **AN. CG56054-05: Integrin alpha 7-like protein.**

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Expression of gene CG56054-05 was assessed using the primer-probe set Ag6436, described in Table ANA.

Table ANA. Probe Name Ag6436

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gggcaagattgttacctgtg-3'	20	402	471
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	440	472
Reverse	5'-ccctggatgcccatc-3'	15	466	473

5   **AO. CG56054-06 and CG56054-07: Integrin alpha 7-like protein.**

Expression of gene CG56054-06 and CG56054-07 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6425, Ag6431, Ag6438, Ag6439, Ag6440, Ag6413 and Ag6964, described in Tables AOA, AOB, AOC, AOD, AOE, AOF, AOG, AOH and AOI. Results of the RTQ-PCR runs are shown in Tables AOJ, AOK, AOL, AOM, AON and

10   AOO. Note that CG56054-07 is recognized by probe-primer sets Ag6425 and Ag6440.

Table AOA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	1057	474
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	1079	475
Reverse	5'-aacagcagctctacctccagtt-3'	22	1113	476

Table AOB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	1496	477
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	1535	478
Reverse	5'-gcgcagtccagggtg-3'	15	1621	479

Table AOC. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	2118	480
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	2150	481
Reverse	5'-gccctggatgcccat-3'	15	2169	482

Table AOD. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	1615	483
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	1656	484
Reverse	5'-ccgcgcggtcaaa-3'	13	1682	485

Table AOE. Probe Name Ag6438

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cagttgcagccctgga-3'	16	342	486
Probe	TET-5'-ccaggttccccgtgtgacgttc-3'-TAMRA	22	397	487
Reverse	5'-tcttccaggttacggctca-3'	19	420	488

5   Table AOF. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	1872	489
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	1892	490
Reverse	5'-gaagaatcccatcttccacag-3'	21	1958	491

Table AOG. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No

563

Forward	5'-accatcctgaggaacaactg-3'	20	2075	492
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	2142	493
Reverse	5'-ccctggatgcccatc-3'	15	2168	494

Table AOH. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	695	495
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	746	496
Reverse	5'-gctgttgttccatccacatc-3'	20	788	497

Table AOI. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	1701	498
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	1672	499
Reverse	5'-gccaactgtgtggtgttca-3'	19	1646	500

Table AOJ. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6442, Run 264979298
AD 1 Hippo	23.7	24.8	18.8	21.6	18.9	19.2
AD 2 Hippo	41.2	52.9	28.7	28.9	61.1	49.7
AD 3 Hippo	8.9	6.4	7.5	6.1	9.7	20.4
AD 4 Hippo	14.8	25.5	18.8	17.6	23.3	5.6
AD 5 Hippo	44.8	41.8	38.4	42.6	34.6	57.4
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	90.1

Control 2 Hippo	24.3	36.1	29.5	32.5	29.9	28.5
Control 4 Hippo	42.9	43.8	32.3	37.9	54.7	86.5
Control (Path) 3 Hippo	14.2	11.4	6.0	6.4	5.8	0.0
AD 1 Temporal Ctx	23.3	15.9	17.1	24.5	12.6	16.8
AD 2 Temporal Ctx	41.5	47.3	39.8	27.5	59.0	21.6
AD 3 Temporal Ctx	9.5	9.8	11.3	9.0	17.1	5.7
AD 4 Temporal Ctx	30.6	39.0	25.3	30.4	29.9	8.7
AD 5 Inf Temporal Ctx	45.4	37.1	36.3	41.8	41.8	73.7
AD 5 Sup Temporal Ctx	51.1	39.0	32.3	38.7	39.2	55.9
AD 6 Inf Temporal Ctx	38.2	59.9	46.7	47.6	48.6	76.8
AD 6 Sup Temporal Ctx	43.8	48.6	50.3	50.3	17.0	59.9
Control 1 Temporal Ctx	12.2	23.0	15.6	24.0	23.3	46.7
Control 2 Temporal Ctx	14.2	32.5	17.4	14.9	43.5	50.0
Control 3 Temporal Ctx	15.1	15.3	14.5	16.5	9.2	9.5
Control 3 Temporal Ctx	23.7	25.0	13.1	23.8	30.1	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	30.6	39.8	51.1	46.0
Control (Path) 2 Temporal Ctx	24.5	25.9	20.4	24.8	7.2	0.0
Control (Path) 3 Temporal Ctx	11.7	16.0	10.9	11.9	9.9	31.0

Control (Path) 4 Temporal Ctx	21.9	27.4	18.2	21.6	14.9	39.5
AD 1 Occipital Ctx	16.0	11.9	11.5	16.0	5.8	6.3
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	8.8	10.2	7.8	4.9
AD 4 Occipital Ctx	18.9	23.7	17.9	18.6	35.4	11.1
AD 5 Occipital Ctx	24.8	28.3	22.5	22.7	16.6	42.3
AD 6 Occipital Ctx	20.6	31.9	17.0	22.1	23.5	14.8
Control 1 Occipital Ctx	9.5	14.4	8.7	7.2	15.2	8.8
Control 2 Occipital Ctx	31.9	42.6	33.2	29.3	35.8	82.4
Control 3 Occipital Ctx	18.8	13.0	17.1	19.2	4.4	8.8
Control 4 Occipital Ctx	18.2	17.0	12.6	13.6	12.9	24.0
Control (Path) 1 Occipital Ctx	38.2	52.5	36.1	39.5	22.4	100.0
Control (Path) 2 Occipital Ctx	9.6	14.1	7.9	7.0	5.0	9.3
Control (Path) 3 Occipital Ctx	4.8	8.7	6.0	5.9	6.7	4.1
Control (Path) 4 Occipital Ctx	16.2	13.2	10.2	11.4	11.9	32.8
Control 1 Parietal Ctx	14.4	21.9	16.3	15.7	33.2	9.2
Control 2 Parietal Ctx	32.8	28.9	28.3	37.1	17.4	28.1
Control 3 Parietal Ctx	20.6	19.8	8.7	10.8	21.6	9.1
Control (Path) 1 Parietal Ctx	35.4	62.4	39.2	37.9	47.3	69.3

Control (Path) 2 Parietal Ctx	22.1	23.8	22.5	18.7	17.1	37.6
Control (Path) 3 Parietal Ctx	11.2	15.4	7.1	12.0	11.7	10.4
Control (Path) 4 Parietal Ctx	31.2	34.2	8.8	27.9	29.3	27.5

<u>Table AOK</u>. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4

Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	**100.0**
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table AOL. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5

Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AOM. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6438, Run 277223173	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	2.6	17.4	13.8	25.0	17.3	3.7	18.8
Melanoma * Hs688(A).T	0.5	0.0	0.8	0.9	0.0	0.4	0.0	0.7
Melanoma * Hs688(B).T	2.7	0.2	2.5	2.2	0.0	2.9	0.8	2.4
Melanoma * M14	0.3	0.0	0.4	0.4	0.0	0.4	0.0	0.7
Melanoma * LOXIMVI	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1
Melanoma * SK-MEL-5	15.2	2.2	18.2	14.6	29.5	18.3	3.0	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.2	0.0	0.0	0.0	0.1
Testis Pool	5.2	3.5	10.4	9.0	4.6	9.1	3.0	9.9
Prostate ca.* (bone met) PC-3	1.9	0.5	1.9	1.8	0.0	1.3	1.2	4.3
Prostate Pool	8.1	1.0	11.3	12.1	7.7	28.5	2.1	10.0
Placenta	0.5	0.0	0.1	0.1	0.0	0.5	0.0	0.4
Uterus Pool	2.2	1.5	4.6	4.5	0.0	5.3	2.3	4.1
Ovarian ca. OVCAR-3	0.9	0.3	0.7	1.1	0.0	1.6	0.4	4.0
Ovarian ca. SK-OV-3	0.8	0.2	0.8	0.9	0.0	1.3	0.5	1.7

Ovarian ca. OVCAR-4	0.2	0.0	0.4	0.8	0.0	0.9	0.0	0.5
Ovarian ca. OVCAR-5	1.6	1.3	1.3	1.7	0.0	1.4	4.2	7.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	84.7	97.9	3.5	69.3	**100.0**	75.8
Ovarian ca. OVCAR-8	13.6	21.9	15.6	14.6	0.0	17.3	18.2	16.7
Ovary	2.7	0.3	3.1	2.3	0.8	2.8	0.8	2.4
Breast ca. MCF-7	0.3	0.0	0.1	0.2	0.0	0.5	0.3	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.2	0.2	0.0	0.2	0.0	0.3
Breast ca. BT 549	0.5	0.0	0.1	0.5	0.0	0.6	0.0	0.4
Breast ca. T47D	0.0	0.0	0.2	0.3	0.0	0.4	0.3	0.5
Breast ca. MDA-N	0.6	0.0	0.6	0.6	0.0	0.6	0.3	0.8
Breast Pool	15.0	4.1	14.6	10.7	21.9	12.2	3.5	16.7
Trachea	4.5	0.7	4.8	4.2	9.7	4.7	1.4	5.6
Lung	2.8	0.7	4.2	3.2	0.0	3.9	5.3	5.1
Fetal Lung	3.9	0.3	5.0	4.8	7.4	5.3	2.9	6.1
Lung ca. NCI-N417	2.0	0.9	3.3	2.6	0.0	4.0	2.0	2.3
Lung ca. LX-1	3.5	2.7	5.0	3.5	0.0	4.9	6.3	44.1
Lung ca. NCI-H146	0.1	0.0	0.1	0.2	0.0	0.1	0.0	0.1
Lung ca. SHP-77	4.0	0.4	5.3	4.5	0.0	4.5	0.8	3.8
Lung ca. A549	0.3	2.6	0.0	0.4	0.0	0.6	2.2	4.7

Lung ca. NCI-H526	0.2	0.0	0.6	0.3	0.0	0.4	0.3	0.5
Lung ca. NCI-H23	2.9	1.0	4.8	3.2	0.0	2.9	2.3	10.3
Lung ca. NCI-H460	0.0	0.0	0.1	0.3	0.0	0.0	0.0	0.3
Lung ca. HOP-62	0.5	0.0	1.0	0.6	0.0	0.5	0.0	0.7
Lung ca. NCI-H522	1.7	0.6	1.7	1.3	0.0	3.3	2.5	8.9
Liver	0.1	0.0	0.0	0.0	0.0	0.1	0.4	2.0
Fetal Liver	0.3	0.3	0.6	0.5	0.0	0.8	0.8	8.2
Liver ca. HepG2	0.1	0.3	0.0	0.2	0.0	0.1	0.9	2.4
Kidney Pool	27.9	0.0	33.9	28.1	100.0	43.2	14.6	32.8
Fetal Kidney	1.4	0.0	4.1	4.0	2.4	5.8	3.4	11.5
Renal ca. 786-0	0.2	0.0	0.3	0.1	0.0	0.3	0.0	0.9
Renal ca. A498	0.0	1.8	0.0	0.3	0.0	0.5	3.8	8.5
Renal ca. ACHN	1.5	0.5	1.7	1.5	0.9	1.2	0.5	2.5
Renal ca. UO-31	0.3	0.0	0.2	0.2	0.0	0.6	0.0	0.3
Renal ca. TK-10	1.9	0.4	2.0	1.9	0.0	2.1	0.5	4.6
Bladder	4.2	0.0	5.5	5.1	6.1	8.3	0.9	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	0.9	1.2	0.0	1.1	0.8	6.7
Gastric ca. KATO III	0.4	0.5	0.2	0.3	0.0	0.4	0.4	0.9
Colon ca. SW-948	0.0	1.5	0.2	0.2	0.0	0.3	2.2	1.2
Colon ca. SW480	20.9	5.2	27.0	23.3	42.3	23.0	6.3	33.7

Colon ca.* (SW480 met) SW620	13.3	4.8	12.8	10.3	8.8	6.1	7.2	25.0
Colon ca. HT29	0.2	0.0	0.2	0.2	0.0	0.0	0.3	0.3
Colon ca. HCT-116	2.1	0.2	2.5	2.0	0.0	2.1	0.6	4.3
Colon ca. CaCo-2	15.0	3.6	19.1	16.7	31.4	18.3	6.5	38.2
Colon cancer tissue	9.0	3.3	11.9	7.6	6.3	7.7	4.4	20.4
Colon ca. SW1116	1.3	3.0	2.0	1.5	0.0	1.8	2.1	6.0
Colon ca. Colo-205	0.1	0.4	0.2	0.0	0.0	0.2	1.3	0.8
Colon ca. SW-48	0.8	3.6	1.5	1.5	0.0	1.4	3.0	2.6
Colon Pool	20.3	5.0	23.2	18.7	22.7	25.5	8.1	20.6
Small Intestine Pool	14.0	1.7	11.2	13.0	3.7	12.8	2.0	10.4
Stomach Pool	8.1	2.3	9.5	9.3	15.0	8.5	4.2	10.7
Bone Marrow Pool	6.8	1.6	10.2	8.7	7.1	18.7	3.5	12.5
Fetal Heart	10.1	2.3	24.5	21.8	44.4	33.7	8.6	20.7
Heart Pool	28.7	7.0	25.9	17.2	4.7	33.7	10.7	26.1
Lymph Node Pool	17.6	6.1	22.1	23.7	50.7	19.9	6.7	24.7
Fetal Skeletal Muscle	31.9	5.2	48.6	46.3	85.9	19.1	19.2	50.7
Skeletal Muscle Pool	17.4	9.2	29.5	25.9	26.1	22.1	22.7	32.3

Spleen Pool	0.9	0.0	2.0	1.7	0.0	2.7	0.6	3.1
Thymus Pool	4.4	2.0	8.1	9.4	16.3	7.7	3.1	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.5	10.7	10.0	2.9	10.9	2.2	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.3	3.8	3.1	0.0	3.8	0.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	2.1	1.0	0.0	1.4	0.5	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.1	0.2	0.0	0.1	0.2	0.1
CNS cancer (astro) SNB-75	8.1	1.1	6.5	10.0	0.0	11.7	2.8	9.7
CNS cancer (glio) SNB-19	79.6	79.0	**100.0**	**100.0**	9.1	**100.0**	97.9	**100.0**
CNS cancer (glio) SF-295	8.2	0.0	8.0	7.8	5.0	8.2	1.5	14.8
Brain (Amygdala) Pool	3.7	0.8	6.2	4.8	6.0	8.0	4.4	5.3
Brain (cerebellum)	12.0	0.4	10.7	9.7	11.8	8.8	1.2	9.7
Brain (fetal)	4.2	0.7	6.6	5.6	8.5	6.8	2.1	6.4

Brain (Hippocampus) Pool	7.5	3.2	8.6	6.9	4.3	11.0	4.3	10.2
Cerebral Cortex Pool	9.7	0.6	7.5	0.7	3.4	11.6	2.0	8.7
Brain (Substantia nigra) Pool	7.4	2.2	10.4	4.7	5.8	10.0	2.0	9.3
Brain (Thalamus) Pool	7.6	2.7	9.3	0.2	22.5	9.7	2.8	8.7
Brain (whole)	6.1	0.4	5.8	0.3	8.6	5.6	1.9	8.7
Spinal Cord Pool	10.1	2.3	11.0	7.6	27.4	12.2	4.2	9.0
Adrenal Gland	3.5	0.3	3.9	3.7	3.2	4.8	0.9	4.1
Pituitary gland Pool	0.9	0.0	1.2	1.1	0.0	1.4	0.6	0.5
Salivary Gland	0.9	0.0	1.3	0.9	0.0	1.1	0.0	1.0
Thyroid (female)	2.0	0.3	2.5	2.5	0.0	1.9	1.3	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.7	0.6	0.0	0.7	0.6	2.2
Pancreas Pool	1.2	0.0	1.1	1.6	0.0	3.2	1.0	2.3

Table AON. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.1	0.3	0.0	0.7	0.0
Secondary Th2 act	0.5	0.3	0.0	0.8	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.7	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0

Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.4	0.0
Primary Tr1 act	0.1	0.0	0.0	0.7	0.0
Primary Th1 rest	0.0	0.0	0.0	0.3	1.2
Primary Th2 rest	0.0	0.0	0.0	0.2	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	0.0	2.4	2.6
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	0.7	2.3
CD8 lymphocyte act	0.4	0.9	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.3	0.0
CD4 lymphocyte none	0.1	0.0	0.0	0.4	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	1.2
LAK cells rest	5.6	5.0	2.7	3.8	15.2
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	6.3	9.0
NK Cells IL-2 rest	0.9	0.1	0.0	2.5	1.4
Two Way MLR 3 day	1.4	1.1	0.0	1.3	1.4
Two Way MLR 5 day	4.5	0.9	0.0	0.9	0.0
Two Way MLR 7 day	2.3	0.7	13.2	2.6	3.7
PBMC rest	0.1	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	0.0	0.0

PBMC PHA-L	0.3	0.2	0.0	0.7	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.2	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	8.1	68.8
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	2.7	1.8
Dendritic cells none	5.6	3.1	13.8	5.3	0.0
Dendritic cells LPS	1.6	0.3	0.0	0.7	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.2	0.0
Monocytes rest	0.2	0.0	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	1.8	2.6
Macrophages rest	0.9	1.8	0.0	0.6	0.0
Macrophages LPS	7.5	4.0	0.0	6.3	9.2
HUVEC none	0.1	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.3	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.5	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.4	0.0
HUVEC IL-11	0.0	0.0	0.0	0.3	0.0
Lung Microvascular EC none	0.2	0.3	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0

Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	1.5	0.0
Astrocytes rest	67.8	97.3	100.0	100.0	100.0
Astrocytes TNFalpha + IL-1beta	100.0	100.0	74.2	74.7	95.9
KU-812 (Basophil) rest	0.1	0.0	0.0	0.4	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.8	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	6.7	8.5
NCI-H292 none	0.3	0.3	0.0	0.6	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.5	0.0
NCI-H292 IL-9	0.3	0.0	0.0	0.5	0.0
NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.0
NCI-H292 IFN gamma	0.2	0.0	0.0	0.6	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	65.5	94.0
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	39.8	62.9
Lung fibroblast IL-4	26.1	28.7	19.1	21.2	34.9
Lung fibroblast IL-9	28.5	42.0	23.5	26.8	96.6

Lung fibroblast IL-13	31.6	14.6	4.5	10.4	13.4
Lung fibroblast IFN gamma	20.4	32.8	15.7	46.3	89.5
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.3	4.1
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	0.8	2.3
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	1.3	0.0
Dermal fibroblast IFN gamma	9.3	20.3	8.5	20.2	26.6
Dermal fibroblast IL-4	10.7	14.6	4.1	19.8	25.5
Dermal Fibroblasts rest	24.8	42.3	8.0	46.7	47.3
Neutrophils TNFa+LPS	0.7	0.0	0.0	0.4	0.0
Neutrophils rest	0.1	0.0	0.0	0.3	0.0
Colon	7.9	4.7	4.0	9.5	8.4
Lung	2.2	1.2	0.0	4.6	2.1
Thymus	3.1	0.8	0.0	0.4	2.4
Kidney	4.2	4.4	4.9	9.7	5.2

Table AOO. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1

Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0

Summary: Ag4983/Ag6413/Ag6431/Ag6439/Ag6440/Ag6442 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6425 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric,

colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous

5   cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases,

10   such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as

15   Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

     . **General_screening_panel_v1.5 Summary:** Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be

20   used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for

25   further discussion on the utility of these genes.

     General_screening_panel_v1.6
Summary: Ag6413/Ag6425/Ag6431/Ag6439/Ag6440/Ag6964 Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low

30   levels of expression of this gene is also seen in all the regions of central nervous system,

tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6438 Highest expression is detected in kidney (CTs=32.9). In addition, low levels of expression also seen in fetal heart, lymph node, fetal and adult skeletal muscle, spinal

5   cord and a couple of colon cancer cell lines.

Panel 4.1D Summary: Ag4983/Ag6413/Ag6425/Ag6431/Ag6439 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other

10   inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types

15   and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver

20   cirrhosis.

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore,

25   expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to

30   detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this

gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AP. CG56054-08: Integrin alpha 7-like protein.

Expression of gene CG56054-08 was assessed using the primer-probe sets Ag6424, Ag6425, Ag6426, Ag6430, Ag6439 and Ag6440, described in Tables APA, APB, APC, APD, APE and APF. Results of the RTQ-PCR runs are shown in Tables APG, APH and API.

Table APA. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	501
	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	761	502
Reverse	5'-aaaagcaacccccttccaa-3'	18	824	503

Table APB. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	1592	504
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	1624	505
Reverse	5'-gccctggatgcccat-3'	15	1643	506

Table APC. Probe Name Ag6426

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtcactgggctgggatct-3'	18	1249	507
Probe	TET-5'-ctctccggctctgcggctc-3'-TAMRA	19	1270	508
Reverse	5'-actccttctgccaccaca-3'	18	1347	509

Table APD. Probe Name Ag6430

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Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	843	510
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	866	511
Reverse	5'-gggagccggtcagca-3'	15	899	512

Table APE. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	1346	513
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	1366	514
Reverse	5'-gaagaatcccatcttccacag-3'	21	1432	515

Table APF. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	1549	516
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	1616	517
Reverse	5'-ccctggatgcccatc-3'	15	1642	518

Table APG. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003
AD 1 Hippo	20.0	21.6	18.9
AD 2 Hippo	48.0	28.9	61.1
AD 3 Hippo	11.6	6.1	9.7
AD 4 Hippo	17.1	17.6	23.3
AD 5 hippo	39.2	42.6	34.6
AD 6 Hippo	100.0	100.0	100.0

Control 2 Hippo	17.9	32.5	29.9
Control 4 Hippo	38.4	37.9	54.7
Control (Path) 3 Hippo	10.2	6.4	5.8
AD 1 Temporal Ctx	12.1	24.5	12.6
AD 2 Temporal Ctx	36.6	27.5	59.0
AD 3 Temporal Ctx	11.7	9.0	17.1
AD 4 Temporal Ctx	15.6	30.4	29.9
AD 5 Inf Temporal Ctx	43.8	41.8	41.8
AD 5 SupTemporal Ctx	56.6	38.7	39.2
AD 6 Inf Temporal Ctx	40.9	47.6	48.6
AD 6 Sup Temporal Ctx	44.1	50.3	17.0
Control 1 Temporal Ctx	11.9	24.0	23.3
Control 2 Temporal Ctx	16.7	14.9	43.5
Control 3 Temporal Ctx	13.0	16.5	9.2
Control 4 Temporal Ctx	18.9	23.8	30.1
Control (Path) 1 Temporal Ctx	32.5	39.8	51.1
Control (Path) 2 Temporal Ctx	19.5	24.8	7.2
Control (Path) 3 Temporal Ctx	12.9	11.9	9.9
Control (Path) 4 Temporal Ctx	19.8	21.6	14.9
AD 1 Occipital Ctx	16.2	16.0	5.8
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 3 Occipital Ctx	11.7	10.2	7.8
AD 4 Occipital Ctx	12.6	18.6	35.4
AD 5 Occipital Ctx	16.7	22.7	16.6
AD 6 Occipital Ctx	17.8	22.1	23.5

Control 1 Occipital Ctx	11.3	7.2	15.2
Control 2 Occipital Ctx	24.8	29.3	35.8
Control 3 Occipital Ctx	16.4	19.2	4.4
Control 4 Occipital Ctx	12.1	13.6	12.9
Control (Path) 1 Occipital Ctx	32.8	39.5	22.4
Control (Path) 2 Occipital Ctx	9.6	7.0	5.0
Control (Path) 3 Occipital Ctx	8.4	5.9	6.7
Control (Path) 4 Occipital Ctx	15.9	11.4	11.9
Control 1 Parietal Ctx	15.2	15.7	33.2
Control 2 Parietal Ctx	39.5	37.1	17.4
Control 3 Parietal Ctx	14.5	10.8	21.6
Control (Path) 1 Parietal Ctx	33.4	37.9	47.3
Control (Path) 2 Parietal Ctx	20.0	18.7	17.1
Control (Path) 3 Parietal Ctx	15.0	12.0	11.7
Control (Path) 4 Parietal Ctx	28.3	27.9	29.3

Table APH. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177
Adipose	0.0	2.6	8.2	17.3	3.7
Melanoma* Hs688(A).T	0.0	0.0	0.5	0.4	0.0
Melanoma* Hs688(B).T	0.0	0.2	0.6	2.9	0.8
Melanoma* M14	0.0	0.0	0.7	0.4	0.0
Melanoma* LOXIMVI	0.0	0.0	0.0	0.0	0.0

Melanoma* SK-MEL-5	0.0	2.2	22.5	18.3	3.0
Squamous cell carcinoma SCC-4	0.0	0.0	0.3	0.0	0.0
Testis Pool	0.0	3.5	4.2	9.1	3.0
Prostate ca.* (bone met) PC-3	0.0	0.5	1.0	1.3	1.2
Prostate Pool	0.0	1.0	8.5	28.5	2.1
Placenta	0.0	0.0	0.1	0.5	0.0
Uterus Pool	0.0	1.5	2.6	5.3	2.3
Ovarian ca. OVCAR-3	0.0	0.3	0.8	1.6	0.4
Ovarian ca. SK-OV-3	0.0	0.2	1.5	1.3	0.5
Ovarian ca. OVCAR-4	0.0	0.0	0.5	0.9	0.0
Ovarian ca. OVCAR-5	0.0	1.3	1.5	1.4	4.2
Ovarian ca. IGROV-1	**100.0**	**100.0**	90.8	69.3	**100.0**
Ovarian ca. OVCAR-8	5.6	21.9	11.9	17.3	18.2
Ovary	0.0	0.3	2.1	2.8	0.8
Breast ca. MCF-7	0.0	0.0	0.4	0.5	0.3
Breast ca. MDA-MB-231	0.0	0.0	0.4	0.2	0.0
Breast ca. BT 549	0.0	0.0	0.3	0.6	0.0
Breast ca. T47D	0.0	0.0	0.3	0.4	0.3
Breast ca. MDA-N	0.0	0.0	0.7	0.6	0.3
Breast Pool	0.0	4.1	19.5	12.2	3.5
Trachea	0.0	0.7	2.9	4.7	1.4
Lung	0.0	0.7	1.3	3.9	5.3
Fetal Lung	0.0	0.3	4.0	5.3	2.9
Lung ca. NCI-N417	2.0	0.9	2.7	4.0	2.0
Lung ca. LX-1	3.1	2.7	7.0	4.9	6.3

Lung ca. NCI-H146	0.0	0.0	0.5	0.1	0.0
Lung ca. SHP-77	2.3	0.4	6.3	4.5	0.8
Lung ca. A549	0.0	2.6	0.3	0.6	2.2
Lung ca. NCI-H526	0.0	0.0	0.7	0.4	0.3
Lung ca. NCI-H23	0.0	1.0	4.5	2.9	2.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.0	0.0
Lung ca. HOP-62	0.0	0.0	0.6	0.5	0.0
Lung ca. NCI-H522	0.0	0.6	2.4	3.3	2.5
Liver	0.0	0.0	0.1	0.1	0.4
Fetal Liver	0.0	0.3	0.6	0.8	0.8
Liver ca. HepG2	0.0	0.3	0.1	0.1	0.9
Kidney Pool	6.5	0.0	34.9	43.2	14.6
Fetal Kidney	0.0	0.0	5.1	5.8	3.4
Renal ca. 786-0	0.0	0.0	0.2	0.3	0.0
Renal ca. A498	0.0	1.8	0.1	0.5	3.8
Renal ca. ACHN	0.0	0.5	0.7	1.2	0.5
Renal ca. UO-31	0.0	0.0	0.3	0.6	0.0
Renal ca. TK-10	0.0	0.4	2.5	2.1	0.5
Bladder	0.0	0.0	3.0	8.3	0.9
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.7	1.1	0.8
Gastric ca. KATO III	0.0	0.5	0.4	0.4	0.4
Colon ca. SW-948	0.0	1.5	0.0	0.3	2.2
Colon ca. SW480	9.5	5.2	39.0	23.0	6.3
Colon ca.* (SW480 met) SW620	7.7	4.8	15.5	6.1	7.2
Colon ca. HT29	0.0	0.0	0.0	0.0	0.3
Colon ca. HCT-116	1.6	0.2	3.8	2.1	0.6
Colon ca. CaCo-2	10.4	3.6	22.2	18.3	6.5
Colon cancer tissue	0.0	3.3	6.5	7.7	4.4
Colon ca. SW1116	0.0	3.0	1.7	1.8	2.1
Colon ca. Colo-205	0.0	0.4	0.2	0.2	1.3

Colon ca. SW-48	0.0	3.6	1.3	1.4	3.0
Colon Pool	0.0	5.0	28.7	25.5	8.1
Small Intestine Pool	0.0	1.7	10.5	12.8	2.0
Stomach Pool	0.0	2.3	6.2	8.5	4.2
Bone Marrow Pool	0.0	1.6	11.3	18.7	3.5
Fetal Heart	0.0	2.3	24.3	33.7	8.6
Heart Pool	5.2	7.0	23.0	33.7	10.7
Lymph Node Pool	0.0	6.1	30.4	19.9	6.7
Fetal Skeletal Muscle	36.9	5.2	46.7	19.1	19.2
Skeletal Muscle Pool	12.3	9.2	21.5	22.1	22.7
Spleen Pool	0.0	0.0	2.0	2.7	0.6
Thymus Pool	0.0	2.0	7.5	7.7	3.1
CNS cancer (glio/astro) U87-MG	1.6	1.5	6.1	10.9	2.2
CNS cancer (glio/astro) U-118-MG	0.0	0.3	2.9	3.8	0.8
CNS cancer (neuro;met) SK-N-AS	0.0	0.0	1.7	1.4	0.5
CNS cancer (astro) SF-539	0.0	0.0	0.2	0.1	0.2
CNS cancer (astro) SNB-75	1.9	1.1	5.9	11.7	2.8
CNS cancer (glio) SNB-19	84.1	79.0	100.0	100.0	97.9
CNS cancer (glio) SF-295	1.8	0.0	9.0	8.2	1.5
Brain (Amygdala) Pool	2.3	0.8	6.9	8.0	4.4
Brain (cerebellum)	6.6	0.4	11.1	8.8	1.2
Brain (fetal)	3.0	0.7	11.5	6.8	2.1
Brain (Hippocampus) Pool	3.1	3.2	11.0	11.0	4.3
Cerebral Cortex Pool	1.7	0.6	7.5	11.6	2.0

Brain (Substantia nigra) Pool	1.8	2.2	8.5	10.0	2.0
Brain (Thalamus) Pool	0.0	2.7	10.0	9.7	2.8
Brain (whole)	0.0	0.4	8.0	5.6	1.9
Spinal Cord Pool	3.2	2.3	12.8	12.2	4.2
Adrenal Gland	0.0	0.3	6.1	4.8	0.9
Pituitary gland Pool	0.0	0.0	0.8	1.4	0.6
Salivary Gland	0.0	0.0	1.1	1.1	0.0
Thyroid (female)	0.0	0.3	0.8	1.9	1.3
Pancreatic ca. CAPAN2	0.0	0.0	0.8	0.7	0.6
Pancreas Pool	0.0	0.0	1.1	3.2	1.0

Table API. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0
Primary Th2 act	0.0	0.0	0.0
Primary Tr1 act	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	1.2
Primary Th2 rest	0.0	0.0	0.0
Primary Tr1 rest	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.0	2.6
CD45RO CD4 lymphocyte act	0.0	0.0	2.3

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CD8 lymphocyte act	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	1.2
LAK cells rest	2.7	0.1	15.2
LAK cells IL-2	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	0.1	9.0
NK Cells IL-2 rest	0.0	0.0	1.4
Two Way MLR 3 day	0.0	0.0	1.4
Two Way MLR 5 day	0.0	0.0	0.0
Two Way MLR 7 day	13.2	0.0	3.7
PBMC rest	0.0	0.0	0.0
PBMC PWM	0.0	0.0	0.0
PBMC PHA-L	0.0	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	0.0
EOL-1 dbcAMP	9.1	0.1	68.8
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	1.8
Dendritic cells none	13.8	0.0	0.0
Dendritic cells LPS	0.0	0.0	0.0
Dendritic cells anti-CD40	3.3	0.0	0.0
Monocytes rest	0.0	0.0	0.0

Monocytes LPS	0.0	0.0	2.6
Macrophages rest	0.0	0.0	0.0
Macrophages LPS	0.0	0.1	9.2
HUVEC none	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0
Lung Microvascular EC none	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.0	0.0
Astrocytes rest	**100.0**	12.0	**100.0**
Astrocytes TNFalpha + IL-1beta	74.2	**100.0**	95.9
KU-812 (Basophil) rest	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0

Liver cirrhosis	4.6	0.0	8.5
NCI-H292 none	0.0	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.0	0.0
NCI-H292 IL-13	0.0	0.0	0.0
NCI-H292 IFN gamma	0.0	0.0	0.0
HPAEC none	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0
Lung fibroblast none	31.4	0.2	94.0
Lung fibroblast TNF alpha + IL-1 beta	22.2	0.1	62.9
Lung fibroblast IL-4	19.1	0.1	34.9
Lung fibroblast IL-9	23.5	0.1	96.6
Lung fibroblast IL-13	4.5	0.0	13.4
Lung fibroblast IFN gamma	15.7	0.2	89.5
Dermal fibroblast CCD1070 rest	0.0	0.0	4.1
Dermal fibroblast CCD1070 TNF alpha	0.0	0.0	2.3
Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0	0.0
Dermal fibroblast IFN gamma	8.5	0.1	26.6
Dermal fibroblast IL-4	4.1	0.1	25.5
Dermal Fibroblasts rest	8.0	0.1	47.3
Neutrophils TNFa+LPS	0.0	0.0	0.0
Neutrophils rest	0.0	0.0	0.0
Colon	4.0	0.0	8.4
Lung	0.0	0.0	2.1
Thymus	0.0	0.0	2.4
Kidney	4.9	0.1	5.2

CNS_neurodegeneration_v1.0 Summary: Ag6430/Ag6439/Ag6440 Four experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of

individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

5   General_screening_panel_v1.6
Summary: Ag6424/Ag6425/Ag6430/Ag6439/Ag6440 Five experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low

10   levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D Summary: Ag6425/Ag6430/Ag6439 Three experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected

15   in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by

20   colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

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AQ. CG56054-09: Integrin alpha 7-like protein.

Expression of gene CG56054-09 was assessed using the primer-probe sets Ag6425, Ag6435, Ag6437, Ag6439 and Ag6440, described in Tables AQA, AQB, AQC, AQD and AQE. Results of the RTQ-PCR runs are shown in Tables AQF, AQG and AQH.

30   Table AQA. Probe Name Ag6425

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Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	1240	519
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	1272	520
Reverse	5'-gccctggatgcccat-3'	15	1291	521

Table AQB. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	522
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	523
Reverse	5'-cagggaccgggatga-3'	15	829	524

Table AQC. Probe Name Ag6437

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	525
Probe	TET-5'-cgcctcatcccggtccct-3'-TAMRA	18	825	526
Reverse	5'-ctcctccagaaaggtgctgt-3'	20	847	527

Table AQD. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	994	528
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	1014	529
Reverse	5'-gaagaatcccatcttccacag-3'	21	1080	530

5   Table AQE. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	1197	531

| Probe | TET-5'-ctgacgggcatcccgagct-3'-TAMRA | 19 | 1264 | 532 |
| Reverse | 5'-ccctggatgcccatc-3' | 15 | 1290 | 533 |

Table AQF. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003
AD 1 Hippo	17.1	21.6	18.9
AD 2 Hippo	27.9	28.9	61.1
AD 3 Hippo	4.8	6.1	9.7
AD 4 Hippo	18.3	17.6	23.3
AD 5 Hippo	46.7	42.6	34.6
AD 6 Hippo	**100.0**	100.0	100.0
Control 2 Hippo	8.5	32.5	29.9
Control 4 Hippo	29.9	37.9	54.7
Control (Path) 3 Hippo	5.2	6.4	5.8
AD 1 Temporal Ctx	12.8	24.5	12.6
AD 2 Temporal Ctx	45.1	27.5	59.0
AD 3 Temporal Ctx	4.1	9.0	17.1
AD 4 Temporal Ctx	6.8	30.4	29.9
AD 5 Inf Temporal Ctx	1.6	41.8	41.8
AD 5 Sup Temporal Ctx	33.2	38.7	39.2
AD 6 Inf Temporal Ctx	52.1	47.6	48.6
AD 6 Sup Temporal Ctx	37.6	50.3	17.0
Control 1 Temporal Ctx	6.7	24.0	23.3
Control 2 Temporal Ctx	7.3	14.9	43.5
Control 3 Temporal Ctx	4.4	16.5	9.2
Control 3 Temporal Ctx	11.7	23.8	30.1

Control (Path) 1 Temporal Ctx	24.8	39.8	51.1
Control (Path) 2 Temporal Ctx	9.8	24.8	7.2
Control (Path) 3 Temporal Ctx	3.5	11.9	9.9
Control (Path) 4 Temporal Ctx	14.8	21.6	14.9
AD 1 Occipital Ctx	15.0	16.0	5.8
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 3 Occipital Ctx	8.0	10.2	7.8
AD 4 Occipital Ctx	6.8	18.6	35.4
AD 5 Occipital Ctx	12.7	22.7	16.6
AD 6 Occipital Ctx	5.9	22.1	23.5
Control 1 Occipital Ctx	4.1	7.2	15.2
Control 2 Occipital Ctx	20.3	29.3	35.8
Control 3 Occipital Ctx	7.5	19.2	4.4
Control 4 Occipital Ctx	3.3	13.6	12.9
Control (Path) 1 Occipital Ctx	25.9	39.5	22.4
Control (Path) 2 Occipital Ctx	7.4	7.0	5.0
Control (Path) 3 Occipital Ctx	2.3	5.9	6.7
Control (Path) 4 Occipital Ctx	21.0	11.4	11.9
Control 1 Parietal Ctx	12.5	15.7	33.2
Control 2 Parietal Ctx	41.2	37.1	17.4
Control 3 Parietal Ctx	13.2	10.8	21.6
Control (Path) 1 Parietal Ctx	22.5	37.9	47.3
Control (Path) 2 Parietal Ctx	26.8	18.7	17.1
Control (Path) 3 Parietal Ctx	7.5	12.0	11.7

Control (Path) 4 Parietal Ctx	20.6	27.9	29.3

Table AQG. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177
Adipose	2.6	13.2	17.3	3.7
Melanoma* Hs688(A).T	0.0	0.9	0.4	0.0
Melanoma* Hs688(B).T	0.2	1.9	2.9	0.8
Melanoma* M14	0.0	0.0	0.4	0.0
Melanoma* LOXIMVI	0.0	0.0	0.0	0.0
Melanoma* SK-MEL-5	2.2	4.4	18.3	3.0
Squamous cell carcinoma SCC-4	0.0	0.0	0.0	0.0
Testis Pool	3.5	10.0	9.1	3.0
Prostate ca.* (bone met) PC-3	0.5	1.8	1.3	1.2
Prostate Pool	1.0	10.0	28.5	2.1
Placenta	0.0	0.3	0.5	0.0
Uterus Pool	1.5	16.2	5.3	2.3
Ovarian ca. OVCAR-3	0.3	0.4	1.6	0.4
Ovarian ca. SK-OV-3	0.2	0.9	1.3	0.5
Ovarian ca. OVCAR-4	0.0	0.0	0.9	0.0
Ovarian ca. OVCAR-5	1.3	0.3	1.4	4.2
Ovarian ca. IGROV-1	100.0	27.0	69.3	100.0
Ovarian ca. OVCAR-8	21.9	7.6	17.3	18.2
Ovary	0.3	4.5	2.8	0.8
Breast ca. MCF-7	0.0	0.0	0.5	0.3
Breast ca. MDA-MB-231	0.0	0.0	0.2	0.0
Breast ca. BT 549	0.0	0.0	0.6	0.0
Breast ca. T47D	0.0	0.0	0.4	0.3

Breast ca. MDA-N	0.0	0.7	0.6	0.3
Breast Pool	4.1	42.9	12.2	3.5
Trachea	0.7	8.3	4.7	1.4
Lung	0.7	3.9	3.9	5.3
Fetal Lung	0.3	8.0	5.3	2.9
Lung ca. NCI-N417	0.9	0.2	4.0	2.0
Lung ca. LX-1	2.7	0.9	4.9	6.3
Lung ca. NCI-H146	0.0	0.0	0.1	0.0
Lung ca. SHP-77	0.4	0.2	4.5	0.8
Lung ca. A549	2.6	0.0	0.6	2.2
Lung ca. NCI-H526	0.0	0.0	0.4	0.3
Lung ca. NCI-H23	1.0	0.6	2.9	2.3
Lung ca. NCI-H460	0.0	0.0	0.0	0.0
Lung ca. HOP-62	0.0	0.0	0.5	0.0
Lung ca. NCI-H522	0.6	0.0	3.3	2.5
Liver	0.0	0.0	0.1	0.4
Fetal Liver	0.3	0.3	0.8	0.8
Liver ca. HepG2	0.3	0.0	0.1	0.9
Kidney Pool	0.0	100.0	43.2	14.6
Fetal Kidney	0.0	12.1	5.8	3.4
Renal ca. 786-0	0.0	0.0	0.3	0.0
Renal ca. A498	1.8	0.0	0.5	3.8
Renal ca. ACHN	0.5	0.0	1.2	0.5
Renal ca. UO-31	0.0	0.0	0.6	0.0
Renal ca. TK-10	0.4	0.7	2.1	0.5
Bladder	0.0	6.6	8.3	0.9
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.1	0.8
Gastric ca. KATO III	0.5	0.3	0.4	0.4
Colon ca. SW-948	1.5	0.0	0.3	2.2
Colon ca. SW480	5.2	4.4	23.0	6.3

Colon ca.* (SW480 met) SW620	4.8	1.7	6.1	7.2
Colon ca. HT29	0.0	0.0	0.0	0.3
Colon ca. HCT-116	0.2	0.5	2.1	0.6
Colon ca. CaCo-2	3.6	7.6	18.3	6.5
Colon cancer tissue	3.3	5.6	7.7	4.4
Colon ca. SW1116	3.0	1.1	1.8	2.1
Colon ca. Colo-205	0.4	0.0	0.2	1.3
Colon ca. SW-48	3.6	0.0	1.4	3.0
Colon Pool	5.0	44.8	25.5	8.1
Small Intestine Pool	1.7	26.8	12.8	2.0
Stomach Pool	2.3	24.0	8.5	4.2
Bone Marrow Pool	1.6	25.9	18.7	3.5
Fetal Heart	2.3	31.6	33.7	8.6
Heart Pool	7.0	23.5	33.7	10.7
Lymph Node Pool	6.1	64.6	19.9	6.7
Fetal Skeletal Muscle	5.2	46.7	19.1	19.2
Skeletal Muscle Pool	9.2	24.7	22.1	22.7
Spleen Pool	0.0	2.4	2.7	0.6
Thymus Pool	2.0	18.4	7.7	3.1
CNS cancer (glio/astro) U87-MG	1.5	5.8	10.9	2.2
CNS cancer (glio/astro) U-118-MG	0.3	1.5	3.8	0.8
CNS cancer (neuro;met) SK-N-AS	0.0	0.7	1.4	0.5
CNS cancer (astro) SF-539	0.0	0.2	0.1	0.2
CNS cancer (astro) SNB-75	1.1	3.1	11.7	2.8
CNS cancer (glio) SNB-19	79.0	12.8	**100.0**	97.9
CNS cancer (glio) SF-295	0.0	0.0	8.2	1.5

Brain (Amygdala) Pool	0.8	7.9	8.0	4.4
Brain (cerebellum)	0.4	1.8	8.8	1.2
Brain (fetal)	0.7	8.4	6.8	2.1
Brain (Hippocampus) Pool	3.2	9.9	11.0	4.3
Cerebral Cortex Pool	0.6	1.8	11.6	2.0
Brain (Substantia nigra) Pool	2.2	4.2	10.0	2.0
Brain (Thalamus) Pool	2.7	9.1	9.7	2.8
Brain (whole)	0.4	3.3	5.6	1.9
Spinal Cord Pool	2.3	13.1	12.2	4.2
Adrenal Gland	0.3	7.4	4.8	0.9
Pituitary gland Pool	0.0	1.8	1.4	0.6
Salivary Gland	0.0	2.3	1.1	0.0
Thyroid (female)	0.3	3.3	1.9	1.3
Pancreatic ca. CAPAN2	0.0	0.5	0.7	0.6
Pancreas Pool	0.0	3.5	3.2	1.0

Table AQH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.7	0.0
Secondary Tr1 rest	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0
Primary Th2 act	0.0	0.7	0.0
Primary Tr1 act	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	1.2
Primary Th2 rest	0.0	0.0	0.0

Primary Tr1 rest	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.8	2.6
CD45RO CD4 lymphocyte act	0.0	1.6	2.3
CD8 lymphocyte act	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	1.2
LAK cells rest	2.7	6.1	15.2
LAK cells IL-2	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	6.1	9.0
NK Cells IL-2 rest	0.0	0.0	1.4
Two Way MLR 3 day	0.0	0.9	1.4
Two Way MLR 5 day	0.0	0.0	0.0
Two Way MLR 7 day	13.2	2.9	3.7
PBMC rest	0.0	0.0	0.0
PBMC PWM	0.0	0.0	0.0
PBMC PHA-L	0.0	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	0.0
EOL-1 dbcAMP	9.1	0.0	68.8
EOL-1 dbcAMP PMA/ionomycin	0.0	1.0	1.8
Dendritic cells none	13.8	0.7	0.0

Dendritic cells LPS	0.0	0.0	0.0
Dendritic cells anti-CD40	3.3	1.6	0.0
Monocytes rest	0.0	0.0	0.0
Monocytes LPS	0.0	0.0	2.6
Macrophages rest	0.0	0.0	0.0
Macrophages LPS	0.0	0.8	9.2
HUVEC none	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.6	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0
Lung Microvascular EC none	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.5	0.0
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.0	0.0
Astrocytes rest	**100.0**	**100.0**	**100.0**
Astrocytes TNFalpha + IL-1beta	74.2	97.9	95.9
KU-812 (Basophil) rest	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0

CCD1106 (Keratinocytes) none	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0
Liver cirrhosis	4.6	5.1	8.5
NCI-H292 none	0.0	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.0	0.0
NCI-H292 IL-13	0.0	0.0	0.0
NCI-H292 IFN gamma	0.0	0.0	0.0
HPAEC none	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0
Lung fibroblast none	31.4	62.9	94.0
Lung fibroblast TNF alpha + IL-1 beta	22.2	25.2	62.9
Lung fibroblast IL-4	19.1	23.3	34.9
Lung fibroblast IL-9	23.5	20.4	96.6
Lung fibroblast IL-13	4.5	15.0	13.4
Lung fibroblast IFN gamma	15.7	29.9	89.5
Dermal fibroblast CCD1070 rest	0.0	5.6	4.1
Dermal fibroblast CCD1070 TNF alpha	0.0	0.8	2.3
Dermal fibroblast CCD1070 IL-1 beta	0.0	0.7	0.0
Dermal fibroblast IFN gamma	8.5	20.0	26.6
Dermal fibroblast IL-4	4.1	22.7	25.5
Dermal Fibroblasts rest	8.0	20.7	47.3
Neutrophils TNFa+LPS	0.0	1.2	0.0
Neutrophils rest	0.0	0.0	0.0
Colon	4.0	7.9	8.4
Lung	0.0	1.6	2.1
Thymus	0.0	2.0	2.4
Kidney	4.9	10.2	5.2

CNS_neurodegeneration_v1.0 Summary: Ag6435/Ag6439/Ag6440 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this

5   experiment. See Panel 1.4 for a discussion of the of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6 Summary: Ag6425/ Ag6435/Ag6439/Ag6440 Highest expression of this gene is detected in kidney, ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=28-31). In addition, consistent with expression seen in

10   panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D Summary:: Ag6425/ Ag6435/Ag6439 Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-34.5). Therefore,

15   therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by

20   colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

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AR. CG56054-10 and CG56054-11:Integrin alpha 7-like protein.

Expression of gene CG56054-10 and CG56054-11 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6425, Ag6428, Ag6431, Ag6433, Ag6435, Ag6440, Ag6446, Ag6447, Ag6413 and Ag6964, described in Tables ARA, ARB, ARC, ARD, ARE,

30   ARF, ARG, ARH, ARI, ARJ, ARK and ARL. Results of the RTQ-PCR runs are shown in Tables ARM, ARN, ARO, ARP, ARQ and ARR. Note Ag6433 is specific for CG56054-11.

Also, the CG56054-11 gene is only recognized by probe-primer sets Ag6433, Ag6431, Ag6446 and Ag6964.

Table ARA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2342	534
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2364	535
Reverse	5'-aacagcagctctacctccagtt-3'	22	2398	536

5

Table ARB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2781	537
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2820	538
Reverse	5'-gcgcagtccagggtg-3'	15	2906	539

Table ARC. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	3516	540
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	3548	541
Reverse	5'-gccctggatgcccat-3'	15	3567	542

Table ARD. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	543
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	544

Reverse	5'-agggagtagccgaagctct-3'	19	1378	545

Table ARE. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2900	546
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2941	547
Reverse	5'-ccgcgcggtcaaa-3'	13	2967	548

Table ARF. Probe Name Ag6433

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggagtcagtgtcctctgctga-3'	21	534	549
Probe	TET-5'-ctgcccactctacagctttgaccgc-3'-TAMRA	25	615	550
Reverse	5'-cccagacatgcagcacag-3'	18	644	551

Table ARG. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	552
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	553
Reverse	5'-cagggaccgggatga-3'	15	829	554

Table ARH. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	3473	555
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	3540	556
Reverse	5'-ccctggatgcccatc-3'	15	3566	557

Table ARI. Probe Name Ag6446

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Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gcttcttccatcggagca-3'	18	3256	558
Probe	TET-5'-caactatcaccgggcctgtctggc-3'-TAMRA	24	3296	559
Reverse	5'-catggctgaaggctgca-3'	17	3322	560

Table ARJ. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	561
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	562
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	563

Table ARK. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	1980	564
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2031	565
Reverse	5'-gctgttgttccatccacatc-3'	20	2073	566

Table ARL. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2986	567
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2957	568
Reverse	5'-gccaactgtgtggtgttca-3'	19	2931	569

5   Table ARM. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6433, Run 268030711	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6442, Run 264979298	Rel. Exp.(%) Ag6446, Run 269254006	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	23.7	24.8	18.0	18.8	27.0	17.1	18.9	19.2	42.9	18.8
AD 2 Hippo	41.2	52.9	32.3	28.7	43.5	27.9	61.1	49.7	41.8	10.4
AD 3 Hippo	8.9	6.4	3.7	7.5	9.9	4.8	9.7	20.4	23.7	0.0
AD 4 Hippo	14.8	25.5	10.7	18.8	18.2	18.3	23.3	5.6	29.9	4.6
AD 5 Hippo	44.8	41.8	53.2	38.4	44.8	46.7	34.6	57.4	67.8	11.0
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.1	100.0	100.0
Control 2 Hippo	24.3	36.1	18.7	29.5	20.7	8.5	29.9	28.5	39.2	3.1
Control 4 Hippo	42.9	43.8	27.0	32.3	52.1	29.9	54.7	86.5	62.4	43.8
Control (Path) 3 Hippo	14.2	11.4	4.6	6.0	6.8	5.2	5.8	0.0	14.6	5.3
AD 1 Temporal Ctx	23.3	15.9	12.9	17.1	23.7	12.8	12.6	16.8	72.7	9.0
AD 2 Temporal Ctx	41.5	47.3	31.0	39.8	24.7	45.1	59.0	21.6	43.2	21.0
AD 3 Temporal Ctx	9.5	9.8	6.0	11.3	11.5	4.1	17.1	5.7	36.3	3.9
AD 4 Temporal Ctx	30.6	39.0	20.2	25.3	19.1	6.8	29.9	8.7	43.2	7.7
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	36.3	30.6	1.6	41.8	73.7	63.3	23.7

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AD 5 Sup Temporal Ctx	51.1	39.0	42.0	32.3	38.7	33.2	39.2	55.9	95.3	11.4
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	46.7	43.5	52.1	48.6	76.8	45.1	88.9
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	50.3	62.0	37.6	17.0	59.9	30.6	61.1
Control 1 Temporal Ctx	12.2	23.0	12.9	15.6	11.8	6.7	23.3	46.7	5.9	2.8
Control 2 Temporal Ctx	14.2	32.5	18.2	17.4	31.0	7.3	43.5	50.0	13.6	16.0
Control 3 Temporal Ctx	15.1	15.3	9.6	14.5	12.6	4.4	9.2	9.5	12.5	3.1
Control 3 Temporal Ctx	23.7	25.0	15.2	13.1	17.7	11.7	30.1	13.6	26.6	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	30.6	39.2	24.8	51.1	46.0	21.2	13.8
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	20.4	14.2	9.8	7.2	0.0	27.2	2.6
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	10.9	13.6	3.5	9.9	31.0	24.5	6.3
Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	18.2	11.9	14.8	14.9	39.5	19.2	7.0

AD 1 Occipital Ctx	16.0	11.9	10.2	11.5	13.1	15.0	5.8	6.3	39.5	0.0
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	8.8	8.0	8.0	7.8	4.9	19.3	0.0
AD 4 Occipital Ctx	18.9	23.7	13.0	17.9	15.9	6.8	35.4	11.1	25.3	3.5
AD 5 Occipital Ctx	24.8	28.3	25.3	22.5	36.6	12.7	16.6	42.3	25.2	3.8
AD 6 Occipital Ctx	20.6	31.9	20.2	17.0	16.0	5.9	23.5	14.8	9.7	8.5
Control 1 Occipital Ctx	9.5	14.4	6.0	8.7	15.1	4.1	15.2	8.8	6.5	1.3
Control 2 Occipital Ctx	31.9	42.6	26.4	33.2	25.0	20.3	35.8	82.4	8.1	13.7
Control 3 Occipital Ctx	18.8	13.0	10.7	17.1	12.1	7.5	4.4	8.8	15.8	5.0
Control 4 Occipital Ctx	18.2	17.0	12.0	12.6	14.4	3.3	12.9	24.0	23.3	1.3
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	36.1	40.9	25.9	22.4	**100.0**	23.3	12.1
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	7.9	6.3	7.4	5.0	9.3	15.6	13.2

Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	6.0	5.3	2.3	6.7	4.1	4.5	9.4
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	10.2	5.8	21.0	11.9	32.8	5.9	20.4
Control 1 Parietal Ctx	14.4	21.9	8.8	16.3	13.2	12.5	33.2	9.2	5.7	5.0
Control 2 Parietal Ctx	32.8	28.9	34.4	28.3	27.4	41.2	17.4	28.1	74.2	25.5
Control 3 Parietal Ctx	20.6	19.8	11.5	8.7	18.2	13.2	21.6	9.1	8.6	16.7
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	39.2	44.1	22.5	47.3	69.3	24.0	4.2
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	22.5	16.5	26.8	17.1	37.6	23.7	14.4
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	7.1	8.7	7.5	11.7	10.4	11.0	5.9
Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	8.8	14.0	20.6	29.3	27.5	27.0	9.4

Table ARN. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0

Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2

Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	100.0
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table ARO. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1

Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4

Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table ARP. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6433, Run 277222449	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6440, Run 277223177	Rel. Exp.(%) Ag6446, Run 277250179	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	2.6	20.0	17.4	13.8	19.5	13.2	3.7	1.7	18.8
Melanoma* Hs688(A).T	0.5	0.0	2.0	0.8	0.9	0.3	0.9	0.0	0.1	0.7
Melanoma* Hs688(B).T	2.7	0.2	4.1	2.5	2.2	2.5	1.9	0.8	0.1	2.4
Melanoma* M14	0.3	0.0	0.7	0.4	0.4	0.5	0.0	0.0	0.1	0.7
Melanoma* LOXIMVI	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	0.1	0.1
Melanoma* SK-MEL-5	15.2	2.2	30.4	18.2	14.6	13.1	4.4	3.0	6.8	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.1	0.2	0.1	0.0	0.0	0.0	0.1
Testis Pool	5.2	3.5	8.8	10.4	9.0	10.4	10.0	3.0	5.8	9.9
Prostate ca.* (bone met) PC-3	1.9	0.5	2.5	1.9	1.8	1.5	1.8	1.2	7.7	4.3
Prostate Pool	8.1	1.0	11.5	11.3	12.1	15.0	10.0	2.1	1.9	10.0
Placenta	0.5	0.0	0.7	0.1	0.1	0.5	0.3	0.0	0.9	0.4
Uterus Pool	2.2	1.5	4.5	4.6	4.5	4.7	16.2	2.3	0.3	4.1

Ovarian ca. OVCAR-3	0.9	0.3	1.1	0.7	1.1	0.9	0.4	0.4	4.8	4.0
Ovarian ca. SK-OV-3	0.8	0.2	1.7	0.8	0.9	1.2	0.9	0.5	2.5	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.9	0.4	0.8	0.3	0.0	0.0	0.5	0.5
Ovarian ca. OVCAR-5	1.6	1.3	2.9	1.3	1.7	2.1	0.3	4.2	15.6	7.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	77.9	84.7	97.9	**100.0**	27.0	**100.0**	5.4	75.8
Ovarian ca. OVCAR-8	13.6	21.9	14.0	15.6	14.6	17.1	7.6	18.2	4.2	16.7
Ovary	2.7	0.3	5.2	3.1	2.3	4.1	4.5	0.8	0.2	2.4
Breast ca. MCF-7	0.3	0.0	0.3	0.1	0.2	0.1	0.0	0.3	0.9	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.4	0.2	0.2	0.1	0.0	0.0	0.2	0.3
Breast ca. BT 549	0.5	0.0	0.5	0.1	0.5	0.6	0.0	0.0	0.2	0.4
Breast ca. T47D	0.0	0.0	0.5	0.2	0.3	0.4	0.0	0.3	0.7	0.5
Breast ca. MDA-N	0.6	0.0	0.7	0.6	0.6	1.0	0.7	0.3	0.0	0.8
Breast Pool	15.0	4.1	21.8	14.6	10.7	15.5	42.9	3.5	2.0	16.7
Trachea	4.5	0.7	8.4	4.8	4.2	4.6	8.3	1.4	0.5	5.6
Lung	2.8	0.7	2.3	4.2	3.2	5.2	3.9	5.3	0.5	5.1

Fetal Lung	3.9	0.3	9.1	5.0	4.8	5.1	8.0	2.9	0.5	6.1
Lung ca. NCI-N417	2.0	0.9	3.5	3.3	2.6	2.3	0.2	2.0	0.4	2.3
Lung ca. LX-1	3.5	2.7	6.5	5.0	3.5	4.1	0.9	6.3	**100.0**	44.1
Lung ca. NCI-H146	0.1	0.0	0.3	0.1	0.2	0.3	0.0	0.0	0.1	0.1
Lung ca. SHP-77	4.0	0.4	6.8	5.3	4.5	6.1	0.2	0.8	0.1	3.8
Lung ca. A549	0.3	2.6	0.9	0.0	0.4	0.7	0.0	2.2	14.3	4.7
Lung ca. NCI-H526	0.2	0.0	0.9	0.6	0.3	0.6	0.0	0.3	0.0	0.5
Lung ca. NCI-H23	2.9	1.0	4.6	4.8	3.2	3.3	0.6	2.3	15.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.1	0.3	0.0	0.0	0.0	0.1	0.3
Lung ca. HOP-62	0.5	0.0	0.5	1.0	0.6	0.6	0.0	0.0	0.2	0.7
Lung ca. NCI-H522	1.7	0.6	2.3	1.7	1.3	1.4	0.0	2.5	27.7	8.9
Liver	0.1	0.0	0.0	0.0	0.0	0.1	0.0	0.4	5.3	2.0
Fetal Liver	0.3	0.3	1.1	0.6	0.5	0.2	0.3	0.8	23.0	8.2
Liver ca. HepG2	0.1	0.3	0.2	0.0	0.2	0.3	0.0	0.9	7.3	2.4
Kidney Pool	27.9	0.0	47.0	33.9	28.1	28.3	**100.0**	14.6	5.3	32.8
Fetal Kidney	1.4	0.0	4.9	4.1	4.0	4.1	12.1	3.4	20.2	11.5
Renal ca. 786-0	0.2	0.0	0.2	0.3	0.1	0.5	0.0	0.0	1.7	0.9
Renal ca. A498	0.0	1.8	0.2	0.0	0.3	0.0	0.0	3.8	23.0	8.5

Renal ca. ACHN	1.5	0.5	2.5	1.7	1.5	2.1	0.0	0.5	3.8	2.5
Renal ca. UO-31	0.3	0.0	0.5	0.2	0.2	0.4	0.0	0.0	0.7	0.3
Renal ca. TK-10	1.9	0.4	3.1	2.0	1.9	2.9	0.7	0.5	6.4	4.6
Bladder	4.2	0.0	5.9	5.5	5.1	4.2	6.6	0.9	3.2	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	1.7	0.9	1.2	1.3	0.0	0.8	17.8	6.7
Gastric ca. KATO III	0.4	0.5	0.8	0.2	0.3	0.2	0.3	0.4	1.3	0.9
Colon ca. SW-948	0.0	1.5	0.2	0.2	0.2	0.0	0.0	2.2	6.1	1.2
Colon ca. SW480	20.9	5.2	41.8	27.0	23.3	26.8	4.4	6.3	39.0	33.7
Colon ca.* (SW480 met) SW620	13.3	4.8	16.4	12.8	10.3	13.0	1.7	7.2	71.2	25.0
Colon ca. HT29	0.2	0.0	0.0	0.2	0.2	0.1	0.0	0.3	3.5	0.3
Colon ca. HCT-116	2.1	0.2	3.2	2.5	2.0	2.3	0.5	0.6	6.4	4.3
Colon ca. CaCo-2	15.0	3.6	27.0	19.1	16.7	16.5	7.6	6.5	78.5	38.2
Colon cancer tissue	9.0	3.3	11.0	11.9	7.6	10.0	5.6	4.4	21.9	20.4
Colon ca. SW1116	1.3	3.0	2.5	2.0	1.5	1.1	1.1	2.1	19.5	6.0
Colon ca. Colo-205	0.1	0.4	0.3	0.2	0.0	0.0	0.0	1.3	3.0	0.8
Colon ca. SW-48	0.8	3.6	1.4	1.5	1.5	1.0	0.0	3.0	4.2	2.6
Colon Pool	20.3	5.0	28.1	23.2	18.7	18.7	44.8	8.1	3.1	20.6

Small Intestine Pool	14.0	1.7	17.1	11.2	13.0	11.4	26.8	2.0	2.5	10.4
Stomach Pool	8.1	2.3	14.3	9.5	9.3	9.5	24.0	4.2	1.1	10.7
Bone Marrow Pool	6.8	1.6	14.3	10.2	8.7	16.6	25.9	3.5	1.1	12.5
Fetal Heart	10.1	2.3	25.5	24.5	21.8	21.6	31.6	8.6	2.7	20.7
Heart Pool	28.7	7.0	29.7	25.9	17.2	29.7	23.5	10.7	3.4	26.1
Lymph Node Pool	17.6	6.1	33.7	22.1	23.7	23.0	64.6	6.7	2.8	24.7
Fetal Skeletal Muscle	31.9	5.2	54.3	48.6	46.3	47.0	46.7	19.2	57.0	50.7
Skeletal Muscle Pool	17.4	9.2	29.3	29.5	25.9	34.2	24.7	22.7	24.3	32.3
Spleen Pool	0.9	0.0	1.9	2.0	1.7	1.4	2.4	0.6	2.6	3.1
Thymus Pool	4.4	2.0	10.4	8.1	9.4	8.8	18.4	3.1	1.4	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.5	14.9	10.7	10.0	13.2	5.8	2.2	6.3	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.3	4.7	3.8	3.1	3.8	1.5	0.8	5.1	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	2.6	2.1	1.0	2.0	0.7	0.5	3.9	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.1	0.2	0.2	0.2	0.2	0.3	0.1

CNS cancer (astro) SNB-75	8.1	1.1	14.9	6.5	10.0	11.4	3.1	2.8	2.4	9.7
CNS cancer (glio) SNB-19	79.6	79.0	**100.0**	**100.0**	**100.0**	98.6	12.8	97.9	5.2	**100.0**
CNS cancer (glio) SF-295	8.2	0.0	11.3	8.0	7.8	5.9	0.0	1.5	14.9	14.8
Brain (Amygdala) Pool	3.7	0.8	7.7	6.2	4.8	6.0	7.9	4.4	1.1	5.3
Brain (cerebellum)	12.0	0.4	19.8	10.7	9.7	11.5	1.8	1.2	1.4	9.7
Brain (fetal)	4.2	0.7	12.7	6.6	5.6	6.2	8.4	2.1	1.1	6.4
Brain (Hippocampus) Pool	7.5	3.2	11.7	8.6	6.9	8.3	9.9	4.3	2.0	10.2
Cerebral Cortex Pool	9.7	0.6	11.0	7.5	0.7	7.0	1.8	2.0	2.0	8.7
Brain (Substantia nigra) Pool	7.4	2.2	11.7	10.4	4.7	10.1	4.2	2.0	1.1	9.3
Brain (Thalamus) Pool	7.6	2.7	13.2	9.3	0.2	8.5	9.1	2.8	3.2	8.7
Brain (whole)	6.1	0.4	10.6	5.8	0.3	4.9	3.3	1.9	1.9	8.7
Spinal Cord Pool	10.1	2.3	14.7	11.0	7.6	12.1	13.1	4.2	2.9	9.0
Adrenal Gland	3.5	0.3	9.9	3.9	3.7	6.4	7.4	0.9	0.7	4.1
Pituitary gland Pool	0.9	0.0	1.1	1.2	1.1	0.8	1.8	0.6	0.4	0.5

Salivary Gland	0.9	0.0	1.8	1.3	0.9	1.3	2.3	0.0	0.2	1.0
Thyroid (female)	2.0	0.3	3.1	2.5	2.5	3.5	3.3	1.3	0.8	2.3
Pancreati c ca. CAPAN2	0.5	0.0	0.8	0.7	0.6	1.0	0.5	0.6	4.6	2.2
Pancreas Pool	1.2	0.0	2.0	1.1	1.6	1.7	3.5	1.0	2.6	2.3

Table ARQ. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6433, Run 268713319	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6446, Run 268761804	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.1	0.3	0.0	1.3	0.7	0.6	0.0	0.0	0.0
Secondary Th2 act	0.5	0.3	0.0	1.2	0.8	0.6	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.7	0.5	0.0	0.0	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.0	0.7	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.4	0.0	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.3	0.4	0.0	0.7	0.0	0.0
Primary Tr1 act	0.1	0.0	0.0	0.7	0.7	0.0	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	0.0	0.1	0.3	0.0	0.0	0.4	0.0
Primary Th2 rest	0.0	0.0	0.0	0.4	0.2	0.0	0.0	0.0	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0

CD45RA CD4 lymphocyte act	0.4	2.8	0.0	5.4	2.4	0.3	0.8	3.7	0.0
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	1.5	0.7	0.8	1.6	0.0	0.0
CD8 lymphocyte act	0.4	0.9	0.0	0.7	0.0	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	8.8	0.0	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.4	0.3	0.0	0.0	0.0	0.0
CD4 lymphocyte none	0.1	0.0	0.0	0.5	0.4	0.0	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells rest	5.6	5.0	2.7	11.8	3.8	6.4	6.1	19.5	0.0
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0	0.0	1.1	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/iono mycin	4.5	4.0	15.7	15.1	6.3	4.3	6.1	41.5	0.0
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	2.5	0.0	0.0	0.0	0.0

Two Way MLR 3 day	1.4	1.1	0.0	2.2	1.3	0.7	0.9	2.1	0.0
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.9	0.9	0.0	5.8	0.0
Two Way MLR 7 day	2.3	0.7	13.2	1.1	2.6	2.6	2.9	5.8	0.0
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.3	0.0	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.7	0.0	0.0	0.0	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.2	0.0	0.0	0.0	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.6	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	8.1	10.2	0.0	3.6	0.0
EOL-1 dbcAMP PMA/iono mycin	1.6	0.7	0.0	0.0	2.7	1.6	1.0	0.0	0.0
Dendritic cells none	5.6	3.1	13.8	4.1	5.3	4.2	0.7	100.0	0.0
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.7	1.6	0.0	2.4	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.2	0.3	1.6	4.3	0.0
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	1.8	1.0	0.0	1.6	0.4

Macrophages rest	0.9	1.8	0.0	0.6	0.6	1.4	0.0	6.9	0.0
Macrophages LPS	7.5	4.0	0.0	5.4	6.3	2.1	0.8	6.5	0.0
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0	0.6	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.4	0.0	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0	0.4	0.3	0.0	0.0	0.0	0.0
Lung Microvascular EC none	0.2	0.3	0.0	0.4	0.0	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + ILI beta	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.0	0.5	0.0	0.3
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	0.3	1.5	0.5	0.0	0.0	0.0
Astrocytes rest	67.8	97.3	100.0	100.0	100.0	100.0	100.0	1.0	54.3
Astrocytes TNFalpha + IL-1beta	100.0	100.0	74.2	97.3	74.7	65.1	97.9	1.4	100.0
KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.4	0.0	0.0	0.4	0.0
KU-812 (Basophil) PMA/iono mycin	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.8	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	2.6	6.7	2.2	5.1	15.3	0.6
NCI-H292 none	0.3	0.3	0.0	1.7	0.6	0.0	0.0	0.0	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0
NCI-H292 IL-9	0.3	0.0	0.0	0.7	0.5	0.0	0.0	1.4	0.0

NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.9	0.0	0.0	0.9	0.0
NCI-H292 IFN gamma	0.2	0.0	0.0	0.5	0.6	0.6	0.0	0.0	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	1.1	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	95.9	65.5	28.5	62.9	3.1	26.2
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	48.6	39.8	19.3	25.2	0.4	28.3
Lung fibroblast IL-4	26.1	28.7	19.1	27.4	21.2	25.9	23.3	0.9	16.0
Lung fibroblast IL-9	28.5	42.0	23.5	24.0	26.8	25.9	20.4	2.0	9.3
Lung fibroblast IL-13	31.6	14.6	4.5	11.9	10.4	16.0	15.0	1.3	4.3
Lung fibroblast IFN gamma	20.4	32.8	15.7	55.9	46.3	25.0	29.9	1.0	25.2
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.0	6.3	2.3	5.6	1.1	0.0
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	2.7	0.8	5.1	0.8	0.0	1.1
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	5.6	1.3	1.4	0.7	0.0	1.6
Dermal fibroblast IFN gamma	9.3	20.3	8.5	30.6	20.2	13.6	20.0	0.0	4.9

Dermal fibroblast IL-4	10.7	14.6	4.1	30.8	19.8	13.9	22.7	1.4	13.5
Dermal Fibroblasts rest	24.8	42.3	8.0	54.3	46.7	19.8	20.7	1.6	15.8
Neutrophils TNFa+LPS	0.7	0.0	0.0	0.9	0.4	0.0	1.2	0.0	0.0
Neutrophils rest	0.1	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0
Colon	7.9	4.7	4.0	4.6	9.5	7.0	7.9	1.8	4.8
Lung	2.2	1.2	0.0	2.8	4.6	1.3	1.6	0.8	0.0
Thymus	3.1	0.8	0.0	0.0	0.4	0.0	2.0	0.0	0.0
Kidney	4.2	4.4	4.9	7.8	9.7	5.3	10.2	50.0	0.6

Table ARR. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0

Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0

Summary: Ag4983/Ag6413/Ag6428/Ag6431/Ag6435/Ag6440/Ag6442/Ag6446/ Ag6447
This panel confirms the expression of this gene at low levels in the brains of an independent
group of individuals. However, no differential expression of this gene was detected between
Alzheimer's diseased postmortem brains and those of non-demented controls in this
experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous
system disorders.

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this
gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of
expression of this gene is also seen in a number of cancer cell lines derived from gastric,
colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression
of this gene could be used as a marker to detect the presence of these cancers. Furthermore,
therapeutic modulation of the expression or function of this gene may be effective in the
treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous
cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at
moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal

muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central

5   nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

10   **General_screening_panel_v1.5 Summary:** Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the

15   regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6

20   **Summary:** Ag6413/Ag6425/Ag6428/Ag6430/Ag6431/Ag6440/Ag6442/ Ag6446/Ag6964 Eight experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in kidney, ovarian cancer IGROV-1 cell line, lung cancer LX-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this

25   gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D

Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6433/Ag6439/Ag6442 Highest

30   expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics

with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by
5   colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

10   Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest
15   expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this
20   gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

25   **AS. CG56054-12: Integrin alpha 7-like protein.**

Expression of gene CG56054-12 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6424, Ag6425, Ag6428, Ag6430, Ag6431, Ag6439, Ag6413 and Ag6964, described in Tables ASA, ASB, ASC, ASD, ASE, ASF, ASG, ASH, ASI and ASJ. Results of the RTQ-PCR runs are shown in Tables ASK, ASL, ASM, ASN, ASO and ASP.

30   Table ASA. Probe Name Ag4983

633

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2435	570
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2457	571
Reverse	5'-aacagcagctctacctccagtt-3'	22	2491	572

Table ASB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2874	573
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2913	574
Reverse	5'-gcgcagtccagggtg-3'	15	2999	575

Table ASC. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	742	576
Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	761	577
Reverse	5'-aaaagcaaccccttccaa-3'	18	824	578

Table ASD. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	3389	579
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	3421	580
Reverse	5'-gccctggatgcccat-3'	15	3440	581

5   Table ASE. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1394	582

Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1434	583
Reverse	5'-agggagtagccgaagctct-3'	19	1471	584

Table ASF. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	843	585
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	866	586
Reverse	5'-gggagccggtcagca-3'	15	899	587

Table ASG. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2993	588
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	3034	589
Reverse	5'-ccgcgcggtcaaa-3'	13	3060	590

Table ASH. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	3250	591
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	3270	592
Reverse	5'-gaagaatcccatcttccacag-3'	21	3336	593

5   Table ASI. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	2073	594

| Probe | TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA | 21 | 2124 | 595 |
| Reverse | 5'-gctgttgttccatccacatc-3' | 20 | 2166 | 596 |

Table ASJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	3079	597
Probe`	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	3050	598
Reverse	5'-gccaactgtgtggtgttca-3'	19	3024	599

Table ASK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6442, Run 264979298
AD 1 Hippo	23.7	24.8	18.0	20.0	18.8	21.6	19.2
AD 2 Hippo	41.2	52.9	32.3	48.0	28.7	28.9	49.7
AD 3 Hippo	8.9	6.4	3.7	11.6	7.5	6.1	20.4
AD 4 Hippo	14.8	25.5	10.7	17.1	18.8	17.6	5.6
AD 5 Hippo	44.8	41.8	53.2	39.2	38.4	42.6	57.4
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	100.0	90.1
Control 2 Hippo	24.3	36.1	18.7	17.9	29.5	32.5	28.5
Control 4 Hippo	42.9	43.8	27.0	38.4	32.3	37.9	86.5
Control (Path) 3 Hippo	14.2	11.4	4.6	10.2	6.0	6.4	0.0
AD 1 Temporal Ctx	23.3	15.9	12.9	12.1	17.1	24.5	16.8
AD 2 Temporal Ctx	41.5	47.3	31.0	36.6	39.8	27.5	21.6

AD 3 Temporal Ctx	9.5	9.8	6.0	11.7	11.3	9.0	5.7
AD 4 Temporal Ctx	30.6	39.0	20.2	15.6	25.3	30.4	8.7
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	43.8	36.3	41.8	73.7
AD 5 Sup Temporal Ctx	51.1	39.0	42.0	56.6	32.3	38.7	55.9
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	40.9	46.7	47.6	76.8
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	44.1	50.3	50.3	59.9
Control 1 Temporal Ctx	12.2	23.0	12.9	11.9	15.6	24.0	46.7
Control 2 Temporal Ctx	14.2	32.5	18.2	16.7	17.4	14.9	50.0
Control 3 Temporal Ctx	15.1	15.3	9.6	13.0	14.5	16.5	9.5
Control 3 Temporal Ctx	23.7	25.0	15.2	18.9	13.1	23.8	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	32.5	30.6	39.8	46.0
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	19.5	20.4	24.8	0.0
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	12.9	10.9	11.9	31.0

Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	19.8	18.2	21.6	39.5
AD 1 Occipital Ctx	16.0	11.9	10.2	16.2	11.5	16.0	6.3
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	11.7	8.8	10.2	4.9
AD 4 Occipital Ctx	18.9	23.7	13.0	12.6	17.9	18.6	11.1
AD 5 Occipital Ctx	24.8	28.3	25.3	16.7	22.5	22.7	42.3
AD 6 Occipital Ctx	20.6	31.9	20.2	17.8	17.0	22.1	14.8
Control 1 Occipital Ctx	9.5	14.4	6.0	11.3	8.7	7.2	8.8
Control 2 Occipital Ctx	31.9	42.6	26.4	24.8	33.2	29.3	82.4
Control 3 Occipital Ctx	18.8	13.0	10.7	16.4	17.1	19.2	8.8
Control 4 Occipital Ctx	18.2	17.0	12.0	12.1	12.6	13.6	24.0
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	32.8	36.1	39.5	100.0
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	9.6	7.9	7.0	9.3
Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	8.4	6.0	5.9	4.1
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	15.9	10.2	11.4	32.8
Control 1 Parietal Ctx	14.4	21.9	8.8	15.2	16.3	15.7	9.2
Control 2 Parietal Ctx	32.8	28.9	34.4	39.5	28.3	37.1	28.1

Control 3 Parietal Ctx	20.6	19.8	11.5	14.5	8.7	10.8	9.1
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	33.4	39.2	37.9	69.3
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	20.0	22.5	18.7	37.6
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	15.0	7.1	12.0	10.4
Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	28.3	8.8	27.9	27.5

Table ASL. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4

Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	100.0
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9

Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table ASM. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3

Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5

Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table ASN. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	0.0	2.6	20.0	8.2	17.4	13.8	17.3	18.8
Melanoma* Hs688(A).T	0.5	0.0	0.0	2.0	0.5	0.8	0.9	0.4	0.7
Melanoma* Hs688(B).T	2.7	0.0	0.2	4.1	0.6	2.5	2.2	2.9	2.4
Melanoma* M14	0.3	0.0	0.0	0.7	0.7	0.4	0.4	0.4	0.7
Melanoma* LOXIMVI	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	15.2	0.0	2.2	30.4	22.5	18.2	14.6	18.3	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.0	0.1	0.3	0.1	0.2	0.0	0.1
Testis Pool	5.2	0.0	3.5	8.8	4.2	10.4	9.0	9.1	9.9
Prostate ca.* (bone met) PC-3	1.9	0.0	0.5	2.5	1.0	1.9	1.8	1.3	4.3
Prostate Pool	8.1	0.0	1.0	11.5	8.5	11.3	12.1	28.5	10.0
Placenta	0.5	0.0	0.0	0.7	0.1	0.1	0.1	0.5	0.4
Uterus Pool	2.2	0.0	1.5	4.5	2.6	4.6	4.5	5.3	4.1
Ovarian ca. OVCAR-3	0.9	0.0	0.3	1.1	0.8	0.7	1.1	1.6	4.0
Ovarian ca. SK-OV-3	0.8	0.0	0.2	1.7	1.5	0.8	0.9	1.3	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.0	0.9	0.5	0.4	0.8	0.9	0.5
Ovarian ca. OVCAR-5	1.6	0.0	1.3	2.9	1.5	1.3	1.7	1.4	7.9

Ovarian ca. IGROV-1	100.0	100.0	100.0	77.9	90.8	84.7	97.9	69.3	75.8
Ovarian ca. OVCAR-8	13.6	5.6	21.9	14.0	11.9	15.6	14.6	17.3	16.7
Ovary	2.7	0.0	0.3	5.2	2.1	3.1	2.3	2.8	2.4
Breast ca. MCF-7	0.3	0.0	0.0	0.3	0.4	0.1	0.2	0.5	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.0	0.4	0.4	0.2	0.2	0.2	0.3
Breast ca. BT 549	0.5	0.0	0.0	0.5	0.3	0.1	0.5	0.6	0.4
Breast ca. T47D	0.0	0.0	0.0	0.5	0.3	0.2	0.3	0.4	0.5
Breast ca. MDA-N	0.6	0.0	0.0	0.7	0.7	0.6	0.6	0.6	0.8
Breast Pool	15.0	0.0	4.1	21.8	19.5	14.6	10.7	12.2	16.7
Trachea	4.5	0.0	0.7	8.4	2.9	4.8	4.2	4.7	5.6
Lung	2.8	0.0	0.7	2.3	1.3	4.2	3.2	3.9	5.1
Fetal Lung	3.9	0.0	0.3	9.1	4.0	5.0	4.8	5.3	6.1
Lung ca. NCI-N417	2.0	2.0	0.9	3.5	2.7	3.3	2.6	4.0	2.3
Lung ca. LX-1	3.5	3.1	2.7	6.5	7.0	5.0	3.5	4.9	44.1
Lung ca. NCI-H146	0.1	0.0	0.0	0.3	0.5	0.1	0.2	0.1	0.1
Lung ca. SHP-77	4.0	2.3	0.4	6.8	6.3	5.3	4.5	4.5	3.8
Lung ca. A549	0.3	0.0	2.6	0.9	0.3	0.0	0.4	0.6	4.7
Lung ca. NCI-H526	0.2	0.0	0.0	0.9	0.7	0.6	0.3	0.4	0.5
Lung ca. NCI-H23	2.9	0.0	1.0	4.6	4.5	4.8	3.2	2.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.0	0.2	0.2	0.1	0.3	0.0	0.3
Lung ca. HOP-62	0.5	0.0	0.0	0.5	0.6	1.0	0.6	0.5	0.7

Lung ca. NCI-H522	1.7	0.0	0.6	2.3	2.4	1.7	1.3	3.3	8.9
Liver	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.1	2.0
Fetal Liver	0.3	0.0	0.3	1.1	0.6	0.6	0.5	0.8	8.2
Liver ca. HepG2	0.1	0.0	0.3	0.2	0.1	0.0	0.2	0.1	2.4
Kidney Pool	27.9	6.5	0.0	47.0	34.9	33.9	28.1	43.2	32.8
Fetal Kidney	1.4	0.0	0.0	4.9	5.1	4.1	4.0	5.8	11.5
Renal ca. 786-0	0.2	0.0	0.0	0.2	0.2	0.3	0.1	0.3	0.9
Renal ca. A498	0.0	0.0	1.8	0.2	0.1	0.0	0.3	0.5	8.5
Renal ca. ACHN	1.5	0.0	0.5	2.5	0.7	1.7	1.5	1.2	2.5
Renal ca. UO-31	0.3	0.0	0.0	0.5	0.3	0.2	0.2	0.6	0.3
Renal ca. TK-10	1.9	0.0	0.4	3.1	2.5	2.0	1.9	2.1	4.6
Bladder	4.2	0.0	0.0	5.9	3.0	5.5	5.1	8.3	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	0.0	1.7	1.7	0.9	1.2	1.1	6.7
Gastric ca. KATO III	0.4	0.0	0.5	0.8	0.4	0.2	0.3	0.4	0.9
Colon ca. SW-948	0.0	0.0	1.5	0.2	0.0	0.2	0.2	0.3	1.2
Colon ca. SW480	20.9	9.5	5.2	41.8	39.0	27.0	23.3	23.0	33.7
Colon ca.* (SW480 met) SW620	13.3	7.7	4.8	16.4	15.5	12.8	10.3	6.1	25.0
Colon ca. HT29	0.2	0.0	0.0	0.0	0.0	0.2	0.2	0.0	0.3
Colon ca. HCT-116	2.1	1.6	0.2	3.2	3.8	2.5	2.0	2.1	4.3
Colon ca. CaCo-2	15.0	10.4	3.6	27.0	22.2	19.1	16.7	18.3	38.2
Colon cancer tissue	9.0	0.0	3.3	11.0	6.5	11.9	7.6	7.7	20.4

Colon ca. SW1116	1.3	0.0	3.0	2.5	1.7	2.0	1.5	1.8	6.0
Colon ca. Colo-205	0.1	0.0	0.4	0.3	0.2	0.2	0.0	0.2	0.8
Colon ca. SW-48	0.8	0.0	3.6	1.4	1.3	1.5	1.5	1.4	2.6
Colon Pool	20.3	0.0	5.0	28.1	28.7	23.2	18.7	25.5	20.6
Small Intestine Pool	14.0	0.0	1.7	17.1	10.5	11.2	13.0	12.8	10.4
Stomach Pool	8.1	0.0	2.3	14.3	6.2	9.5	9.3	8.5	10.7
Bone Marrow Pool	6.8	0.0	1.6	14.3	11.3	10.2	8.7	18.7	12.5
Fetal Heart	10.1	0.0	2.3	25.5	24.3	24.5	21.8	33.7	20.7
Heart Pool	28.7	5.2	7.0	29.7	23.0	25.9	17.2	33.7	26.1
Lymph Node Pool	17.6	0.0	6.1	33.7	30.4	22.1	23.7	19.9	24.7
Fetal Skeletal Muscle	31.9	36.9	5.2	54.3	46.7	48.6	46.3	19.1	50.7
Skeletal Muscle Pool	17.4	12.3	9.2	29.3	21.5	29.5	25.9	22.1	32.3
Spleen Pool	0.9	0.0	0.0	1.9	2.0	2.0	1.7	2.7	3.1
Thymus Pool	4.4	0.0	2.0	10.4	7.5	8.1	9.4	7.7	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.6	1.5	14.9	6.1	10.7	10.0	10.9	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.0	0.3	4.7	2.9	3.8	3.1	3.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	0.0	2.6	1.7	2.1	1.0	1.4	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.0	0.2	0.1	0.2	0.1	0.1

CNS cancer (astro) SNB-75	8.1	1.9	1.1	14.9	5.9	6.5	10.0	11.7	9.7
CNS cancer (glio) SNB-19	79.6	84.1	79.0	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**
CNS cancer (glio) SF-295	8.2	1.8	0.0	11.3	9.0	8.0	7.8	8.2	14.8
Brain (Amygdala) Pool	3.7	2.3	0.8	7.7	6.9	6.2	4.8	8.0	5.3
Brain (cerebellum)	12.0	6.6	0.4	19.8	11.1	10.7	9.7	8.8	9.7
Brain (fetal)	4.2	3.0	0.7	12.7	11.5	6.6	5.6	6.8	6.4
Brain (Hippocampus) Pool	7.5	3.1	3.2	11.7	11.0	8.6	6.9	11.0	10.2
Cerebral Cortex Pool	9.7	1.7	0.6	11.0	7.5	7.5	0.7	11.6	8.7
Brain (Substantia nigra) Pool	7.4	1.8	2.2	11.7	8.5	10.4	4.7	10.0	9.3
Brain (Thalamus) Pool	7.6	0.0	2.7	13.2	10.0	9.3	0.2	9.7	8.7
Brain (whole)	6.1	0.0	0.4	10.6	8.0	5.8	0.3	5.6	8.7
Spinal Cord Pool	10.1	3.2	2.3	14.7	12.8	11.0	7.6	12.2	9.0
Adrenal Gland	3.5	0.0	0.3	9.9	6.1	3.9	3.7	4.8	4.1
Pituitary gland Pool	0.9	0.0	0.0	1.1	0.8	1.2	1.1	1.4	0.5
Salivary Gland	0.9	0.0	0.0	1.8	1.1	1.3	0.9	1.1	1.0
Thyroid (female)	2.0	0.0	0.3	3.1	0.8	2.5	2.5	1.9	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.0	0.8	0.8	0.7	0.6	0.7	2.2

| Pancreas Pool | 1.2 | 0.0 | 0.0 | 2.0 | 1.1 | 1.1 | 1.6 | 3.2 | 2.3 |

Table ASO. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6439, Run 268760823
Secondary Th1 act	0.1	0.3	0.0	1.3	0.7	0.0
Secondary Th2 act	0.5	0.3	0.0	1.2	0.8	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.7	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.4	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.3	0.4	0.0
Primary Tr1 act	0.1	0.0	0.0	0.7	0.7	0.0
Primary Th1 rest	0.0	0.0	0.0	0.1	0.3	1.2
Primary Th2 rest	0.0	0.0	0.0	0.4	0.2	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	0.0	5.4	2.4	2.6
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	1.5	0.7	2.3
CD8 lymphocyte act	0.4	0.9	0.0	0.7	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	8.8	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.4	0.3	0.0
CD4 lymphocyte none	0.1	0.0	0.0	0.5	0.4	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	1.2
LAK cells rest	5.6	5.0	2.7	11.8	3.8	15.2
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0

LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	15.1	6.3	9.0
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	2.5	1.4
Two Way MLR 3 day	1.4	1.1	0.0	2.2	1.3	1.4
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.9	0.0
Two Way MLR 7 day	2.3	0.7	13.2	1.1	2.6	3.7
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.7	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.2	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	8.1	68.8
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	2.7	1.8
Dendritic cells none	5.6	3.1	13.8	4.1	5.3	0.0
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.7	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.2	0.0
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	1.8	2.6
Macrophages rest	0.9	1.8	0.0	0.6	0.6	0.0
Macrophages LPS	7.5	4.0	0.0	5.4	6.3	9.2

HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.3	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.5	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.4	0.0
HUVEC IL-11	0.0	0.0	0.0	0.4	0.3	0.0
Lung Microvascular EC none	0.2	0.3	0.0	0.4	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	0.3	1.5	0.0
Astrocytes rest	67.8	97.3	100.0	100.0	100.0	100.0
Astrocytes TNFalpha + IL-1beta	100.0	100.0	74.2	97.3	74.7	95.9

KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.4	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.8	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	2.6	6.7	8.5
NCI-H292 none	0.3	0.3	0.0	1.7	0.6	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.5	0.0
NCI-H292 IL-9	0.3	0.0	0.0	0.7	0.5	0.0
NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.9	0.0
NCI-H292 IFN gamma	0.2	0.0	0.0	0.5	0.6	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	95.9	65.5	94.0
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	48.6	39.8	62.9
Lung fibroblast IL-4	26.1	28.7	19.1	27.4	21.2	34.9
Lung fibroblast IL-9	28.5	42.0	23.5	24.0	26.8	96.6
Lung fibroblast IL-13	31.6	14.6	4.5	11.9	10.4	13.4
Lung fibroblast IFN gamma	20.4	32.8	15.7	55.9	46.3	89.5
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.0	6.3	4.1
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	2.7	0.8	2.3
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	5.6	1.3	0.0
Dermal fibroblast IFN gamma	9.3	20.3	8.5	30.6	20.2	26.6

Dermal fibroblast IL-4	10.7	14.6	4.1	30.8	19.8	25.5
Dermal Fibroblasts rest	24.8	42.3	8.0	54.3	46.7	47.3
Neutrophils TNFa+LPS	0.7	0.0	0.0	0.9	0.4	0.0
Neutrophils rest	0.1	0.0	0.0	0.0	0.3	0.0
Colon	7.9	4.7	4.0	4.6	9.5	8.4
Lung	2.2	1.2	0.0	2.8	4.6	2.1
Thymus	3.1	0.8	0.0	0.0	0.4	2.4
Kidney	4.2	4.4	4.9	7.8	9.7	5.2

Table ASP. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	100.0	100.0	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9

Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0

Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6424/Ag6425 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases,

5   such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as

10   Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be

15   used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for

20   further discussion on the utility of these genes.

General_screening_panel_v1.6 Summary: Ag6413/Ag6424/ Ag6425/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Eight experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines

25   (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D

30   Summary: Ag4983/Ag6413/Ag6428/Ag6430/Ag6431/Ag6439/Ag6442 Seven experiments with different probe and primer sets are in excellent agreement. Highest

expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

5   In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and
10   inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

15   Ag6424 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in
20   normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding
25   normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

AT. CG56054-13: Integrin alpha 7-like protein.

30   Expression of gene CG56054-13 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6424, Ag6425, Ag6428, Ag6430, Ag6431, Ag6440, Ag6446, Ag6413 and

Ag6964, described in Tables ATA, ATB, ATC, ATD, ATE, ATF, ATG, ATH, ATI, ATJ and ATK. Results of the RTQ-PCR runs are shown in Tables ATL, ATM, ATN, ATO, ATP and ATQ.

Table ATA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2330	600
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2352	601
Reverse	5'-aacagcagctctacctccagtt-3'	22	2386	602

5   Table ATB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2769	603
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2808	604
Reverse	5'-gcgcagtccagggtg-3'	15	2894	605

Table ATC. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	637	606
Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	656	607
Reverse	5'-aaaagcaaccccttccaa-3'	18	719	608

Table ATD. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	3504	609
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	3536	610

| Reverse | 5'-gccctggatgcccat-3' | 15 | 3555 | 611 |

Table ATE. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1289	612
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1329	613
Reverse	5'-agggagtagccgaagctct-3'	19	1366	614

Table ATF. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	738	615
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	761	616
Reverse	5'-gggagccggtcagca-3'	15	794	617

Table ATG. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2888	618
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2929	619
Reverse	5'-ccgcgcggtcaaa-3'	13	2955	620

5   Table ATH. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	3461	621
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	3528	622
Reverse	5'-ccctggatgcccatc-3'	15	3554	623

Table ATI. Probe Name Ag6446

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gcttcttccatcggagca-3'	18	3244	624
Probe	TET-5'-caactatcaccgggcctgtctggc-3'-TAMRA	24	3284	625
Reverse	5'-catggctgaaggctgca-3'	17	3310	626

Table ATJ. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	1968	627
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2019	628
Reverse	5'-gctgttgttccatccacatc-3'	20	2061	629

Table ATK. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2974	630
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2945	631
Reverse	5'-gccaactgtgtggtgttca-3'	19	2919	632

5　　　Table ATL. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6442, Run 264979298	Rel. Exp.(%) Ag6446, Run 269254006
AD 1 Hippo	23.7	24.8	18.0	20.0	18.8	18.9	19.2	42.9
AD 2 Hippo	41.2	52.9	32.3	48.0	28.7	61.1	49.7	41.8

AD 3 Hippo	8.9	6.4	3.7	11.6	7.5	9.7	20.4	23.7
AD 4 Hippo	14.8	25.5	10.7	17.1	18.8	23.3	5.6	29.9
AD 5 Hippo	44.8	41.8	53.2	39.2	38.4	34.6	57.4	67.8
AD 6 Hippo	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	**100.0**	90.1	**100.0**
Control 2 Hippo	24.3	36.1	18.7	17.9	29.5	29.9	28.5	39.2
Control 4 Hippo	42.9	43.8	27.0	38.4	32.3	54.7	86.5	62.4
Control (Path) 3 Hippo	14.2	11.4	4.6	10.2	6.0	5.8	0.0	14.6
AD 1 Temporal Ctx	23.3	15.9	12.9	12.1	17.1	12.6	16.8	72.7
AD 2 Temporal Ctx	41.5	47.3	31.0	36.6	39.8	59.0	21.6	43.2
AD 3 Temporal Ctx	9.5	9.8	6.0	11.7	11.3	17.1	5.7	36.3
AD 4 Temporal Ctx	30.6	39.0	20.2	15.6	25.3	29.9	8.7	43.2
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	43.8	36.3	41.8	73.7	63.3
AD 5 Sup Temporal Ctx	51.1	39.0	42.0	56.6	32.3	39.2	55.9	95.3
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	40.9	46.7	48.6	76.8	45.1
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	44.1	50.3	17.0	59.9	30.6
Control 1 Temporal Ctx	12.2	23.0	12.9	11.9	15.6	23.3	46.7	5.9

Control 2 Temporal Ctx	14.2	32.5	18.2	16.7	17.4	43.5	50.0	13.6
Control 3 Temporal Ctx	15.1	15.3	9.6	13.0	14.5	9.2	9.5	12.5
Control 3 Temporal Ctx	23.7	25.0	15.2	18.9	13.1	30.1	13.6	26.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	32.5	30.6	51.1	46.0	21.2
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	19.5	20.4	7.2	0.0	27.2
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	12.9	10.9	9.9	31.0	24.5
Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	19.8	18.2	14.9	39.5	19.2
AD 1 Occipital Ctx	16.0	11.9	10.2	16.2	11.5	5.8	6.3	39.5
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	11.7	8.8	7.8	4.9	19.3
AD 4 Occipital Ctx	18.9	23.7	13.0	12.6	17.9	35.4	11.1	25.3
AD 5 Occipital Ctx	24.8	28.3	25.3	16.7	22.5	16.6	42.3	25.2
AD 6 Occipital Ctx	20.6	31.9	20.2	17.8	17.0	23.5	14.8	9.7

Control 1 Occipital Ctx	9.5	14.4	6.0	11.3	8.7	15.2	8.8	6.5
Control 2 Occipital Ctx	31.9	42.6	26.4	24.8	33.2	35.8	82.4	8.1
Control 3 Occipital Ctx	18.8	13.0	10.7	16.4	17.1	4.4	8.8	15.8
Control 4 Occipital Ctx	18.2	17.0	12.0	12.1	12.6	12.9	24.0	23.3
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	32.8	36.1	22.4	**100.0**	23.3
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	9.6	7.9	5.0	9.3	15.6
Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	8.4	6.0	6.7	4.1	4.5
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	15.9	10.2	11.9	32.8	5.9
Control 1 Parietal Ctx	14.4	21.9	8.8	15.2	16.3	33.2	9.2	5.7
Control 2 Parietal Ctx	32.8	28.9	34.4	39.5	28.3	17.4	28.1	74.2
Control 3 Parietal Ctx	20.6	19.8	11.5	14.5	8.7	21.6	9.1	8.6
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	33.4	39.2	47.3	69.3	24.0
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	20.0	22.5	17.1	37.6	23.7
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	15.0	7.1	11.7	10.4	11.0

Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	28.3	8.8	29.3	27.5	27.0

Table ATM. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3

Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	**100.0**
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table ATN. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530

Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2

Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table ATO. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6440, Run 277223177	Rel. Exp.(%) Ag6446, Run 277250179	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	0.0	2.6	20.0	8.2	17.4	13.8	3.7	1.7	18.8
Melanoma* Hs688(A).T	0.5	0.0	0.0	2.0	0.5	0.8	0.9	0.0	0.1	0.7

Melanoma* Hs688(B).T	2.7	0.0	0.2	4.1	0.6	2.5	2.2	0.8	0.1	2.4
Melanoma* M14	0.3	0.0	0.0	0.7	0.7	0.4	0.4	0.0	0.1	0.7
Melanoma* LOXIMVI	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1	0.1
Melanoma* SK-MEL-5	15.2	0.0	2.2	30.4	22.5	18.2	14.6	3.0	6.8	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.0	0.1	0.3	0.1	0.2	0.0	0.0	0.1
Testis Pool	5.2	0.0	3.5	8.8	4.2	10.4	9.0	3.0	5.8	9.9
Prostate ca.* (bone met) PC-3	1.9	0.0	0.5	2.5	1.0	1.9	1.8	1.2	7.7	4.3
Prostate Pool	8.1	0.0	1.0	11.5	8.5	11.3	12.1	2.1	1.9	10.0
Placenta	0.5	0.0	0.0	0.7	0.1	0.1	0.1	0.0	0.9	0.4
Uterus Pool	2.2	0.0	1.5	4.5	2.6	4.6	4.5	2.3	0.3	4.1
Ovarian ca. OVCAR-3	0.9	0.0	0.3	1.1	0.8	0.7	1.1	0.4	4.8	4.0
Ovarian ca. SK-OV-3	0.8	0.0	0.2	1.7	1.5	0.8	0.9	0.5	2.5	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.0	0.9	0.5	0.4	0.8	0.0	0.5	0.5
Ovarian ca. OVCAR-5	1.6	0.0	1.3	2.9	1.5	1.3	1.7	4.2	15.6	7.9
Ovarian ca. IGROV-1	100.0	100.0	100.0	77.9	90.8	84.7	97.9	100.0	5.4	75.8
Ovarian ca. OVCAR-8	13.6	5.6	21.9	14.0	11.9	15.6	14.6	18.2	4.2	16.7
Ovary	2.7	0.0	0.3	5.2	2.1	3.1	2.3	0.8	0.2	2.4
Breast ca. MCF-7	0.3	0.0	0.0	0.3	0.4	0.1	0.2	0.3	0.9	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.0	0.4	0.4	0.2	0.2	0.0	0.2	0.3

Breast ca. BT 549	0.5	0.0	0.0	0.5	0.3	0.1	0.5	0.0	0.2	0.4
Breast ca. T47D	0.0	0.0	0.0	0.5	0.3	0.2	0.3	0.3	0.7	0.5
Breast ca. MDA-N	0.6	0.0	0.0	0.7	0.7	0.6	0.6	0.3	0.0	0.8
Breast Pool	15.0	0.0	4.1	21.8	19.5	14.6	10.7	3.5	2.0	16.7
Trachea	4.5	0.0	0.7	8.4	2.9	4.8	4.2	1.4	0.5	5.6
Lung	2.8	0.0	0.7	2.3	1.3	4.2	3.2	5.3	0.5	5.1
Fetal Lung	3.9	0.0	0.3	9.1	4.0	5.0	4.8	2.9	0.5	6.1
Lung ca. NCI-N417	2.0	2.0	0.9	3.5	2.7	3.3	2.6	2.0	0.4	2.3
Lung ca. LX-1	3.5	3.1	2.7	6.5	7.0	5.0	3.5	6.3	**100.0**	44.1
Lung ca. NCI-H146	0.1	0.0	0.0	0.3	0.5	0.1	0.2	0.0	0.1	0.1
Lung ca. SHP-77	4.0	2.3	0.4	6.8	6.3	5.3	4.5	0.8	0.1	3.8
Lung ca. A549	0.3	0.0	2.6	0.9	0.3	0.0	0.4	2.2	14.3	4.7
Lung ca. NCI-H526	0.2	0.0	0.0	0.9	0.7	0.6	0.3	0.3	0.0	0.5
Lung ca. NCI-H23	2.9	0.0	1.0	4.6	4.5	4.8	3.2	2.3	15.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.0	0.2	0.2	0.1	0.3	0.0	0.1	0.3
Lung ca. HOP-62	0.5	0.0	0.0	0.5	0.6	1.0	0.6	0.0	0.2	0.7
Lung ca. NCI-H522	1.7	0.0	0.6	2.3	2.4	1.7	1.3	2.5	27.7	8.9
Liver	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.4	5.3	2.0
Fetal Liver	0.3	0.0	0.3	1.1	0.6	0.6	0.5	0.8	23.0	8.2
Liver ca. HepG2	0.1	0.0	0.3	0.2	0.1	0.0	0.2	0.9	7.3	2.4
Kidney Pool	27.9	6.5	0.0	47.0	34.9	33.9	28.1	14.6	5.3	32.8
Fetal Kidney	1.4	0.0	0.0	4.9	5.1	4.1	4.0	3.4	20.2	11.5

Renal ca. 786-0	0.2	0.0	0.0	0.2	0.2	0.3	0.1	0.0	1.7	0.9
Renal ca. A498	0.0	0.0	1.8	0.2	0.1	0.0	0.3	3.8	23.0	8.5
Renal ca. ACHN	1.5	0.0	0.5	2.5	0.7	1.7	1.5	0.5	3.8	2.5
Renal ca. UO-31	0.3	0.0	0.0	0.5	0.3	0.2	0.2	0.0	0.7	0.3
Renal ca. TK-10	1.9	0.0	0.4	3.1	2.5	2.0	1.9	0.5	6.4	4.6
Bladder	4.2	0.0	0.0	5.9	3.0	5.5	5.1	0.9	3.2	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	0.0	1.7	1.7	0.9	1.2	0.8	17.8	6.7
Gastric ca. KATO III	0.4	0.0	0.5	0.8	0.4	0.2	0.3	0.4	1.3	0.9
Colon ca. SW-948	0.0	0.0	1.5	0.2	0.0	0.2	0.2	2.2	6.1	1.2
Colon ca. SW480	20.9	9.5	5.2	41.8	39.0	27.0	23.3	6.3	39.0	33.7
Colon ca.* (SW480 met) SW620	13.3	7.7	4.8	16.4	15.5	12.8	10.3	7.2	71.2	25.0
Colon ca. HT29	0.2	0.0	0.0	0.0	0.0	0.2	0.2	0.3	3.5	0.3
Colon ca. HCT-116	2.1	1.6	0.2	3.2	3.8	2.5	2.0	0.6	6.4	4.3
Colon ca. CaCo-2	15.0	10.4	3.6	27.0	22.2	19.1	16.7	6.5	78.5	38.2
Colon cancer tissue	9.0	0.0	3.3	11.0	6.5	11.9	7.6	4.4	21.9	20.4
Colon ca. SW1116	1.3	0.0	3.0	2.5	1.7	2.0	1.5	2.1	19.5	6.0
Colon ca. Colo-205	0.1	0.0	0.4	0.3	0.2	0.2	0.0	1.3	3.0	0.8
Colon ca. SW-48	0.8	0.0	3.6	1.4	1.3	1.5	1.5	3.0	4.2	2.6
Colon Pool	20.3	0.0	5.0	28.1	28.7	23.2	18.7	8.1	3.1	20.6

Small Intestine Pool	14.0	0.0	1.7	17.1	10.5	11.2	13.0	2.0	2.5	10.4
Stomach Pool	8.1	0.0	2.3	14.3	6.2	9.5	9.3	4.2	1.1	10.7
Bone Marrow Pool	6.8	0.0	1.6	14.3	11.3	10.2	8.7	3.5	1.1	12.5
Fetal Heart	10.1	0.0	2.3	25.5	24.3	24.5	21.8	8.6	2.7	20.7
Heart Pool	28.7	5.2	7.0	29.7	23.0	25.9	17.2	10.7	3.4	26.1
Lymph Node Pool	17.6	0.0	6.1	33.7	30.4	22.1	23.7	6.7	2.8	24.7
Fetal Skeletal Muscle	31.9	36.9	5.2	54.3	46.7	48.6	46.3	19.2	57.0	50.7
Skeletal Muscle Pool	17.4	12.3	9.2	29.3	21.5	29.5	25.9	22.7	24.3	32.3
Spleen Pool	0.9	0.0	0.0	1.9	2.0	2.0	1.7	0.6	2.6	3.1
Thymus Pool	4.4	0.0	2.0	10.4	7.5	8.1	9.4	3.1	1.4	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.6	1.5	14.9	6.1	10.7	10.0	2.2	6.3	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.0	0.3	4.7	2.9	3.8	3.1	0.8	5.1	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	0.0	2.6	1.7	2.1	1.0	0.5	3.9	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.0	0.2	0.1	0.2	0.2	0.3	0.1
CNS cancer (astro) SNB-75	8.1	1.9	1.1	14.9	5.9	6.5	10.0	2.8	2.4	9.7
CNS cancer (glio) SNB-19	79.6	84.1	79.0	100.0	100.0	100.0	100.0	97.9	5.2	100.0

CNS cancer (glio) SF-295	8.2	1.8	0.0	11.3	9.0	8.0	7.8	1.5	14.9	14.8
Brain (Amygdala) Pool	3.7	2.3	0.8	7.7	6.9	6.2	4.8	4.4	1.1	5.3
Brain (cerebellum)	12.0	6.6	0.4	19.8	11.1	10.7	9.7	1.2	1.4	9.7
Brain (fetal)	4.2	3.0	0.7	12.7	11.5	6.6	5.6	2.1	1.1	6.4
Brain (Hippocampus) Pool	7.5	3.1	3.2	11.7	11.0	8.6	6.9	4.3	2.0	10.2
Cerebral Cortex Pool	9.7	1.7	0.6	11.0	7.5	7.5	0.7	2.0	2.0	8.7
Brain (Substantia nigra) Pool	7.4	1.8	2.2	11.7	8.5	10.4	4.7	2.0	1.1	9.3
Brain (Thalamus) Pool	7.6	0.0	2.7	13.2	10.0	9.3	0.2	2.8	3.2	8.7
Brain (whole)	6.1	0.0	0.4	10.6	8.0	5.8	0.3	1.9	1.9	8.7
Spinal Cord Pool	10.1	3.2	2.3	14.7	12.8	11.0	7.6	4.2	2.9	9.0
Adrenal Gland	3.5	0.0	0.3	9.9	6.1	3.9	3.7	0.9	0.7	4.1
Pituitary gland Pool	0.9	0.0	0.0	1.1	0.8	1.2	1.1	0.6	0.4	0.5
Salivary Gland	0.9	0.0	0.0	1.8	1.1	1.3	0.9	0.0	0.2	1.0
Thyroid (female)	2.0	0.0	0.3	3.1	0.8	2.5	2.5	1.3	0.8	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.0	0.8	0.8	0.7	0.6	0.6	4.6	2.2
Pancreas Pool	1.2	0.0	0.0	2.0	1.1	1.1	1.6	1.0	2.6	2.3

Table ATP. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6431, Run 268767577
Secondary Th1 act	0.1	0.3	0.0	1.3	0.0	0.7
Secondary Th2 act	0.5	0.3	0.0	1.2	0.0	0.8
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.0	0.7
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.4	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.3	0.0	0.4
Primary Tr1 act	0.1	0.0	0.0	0.7	0.0	0.7
Primary Th1 rest	0.0	0.0	0.0	0.1	0.0	0.3
Primary Th2 rest	0.0	0.0	0.0	0.4	0.0	0.2
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	0.0	5.4	0.0	2.4
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	1.5	0.0	0.7
CD8 lymphocyte act	0.4	0.9	0.0	0.7	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	8.8	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.4	0.0	0.3
CD4 lymphocyte none	0.1	0.0	0.0	0.5	0.0	0.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	0.0
LAK cells rest	5.6	5.0	2.7	11.8	0.1	3.8
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0

LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.7	15.1	0.1	6.3
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	0.0	2.5
Two Way MLR 3 day	1.4	1.1	0.0	2.2	0.0	1.3
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.0	0.9
Two Way MLR 7 day	2.3	0.7	13.2	1.1	0.0	2.6
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.0	0.7
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.0	0.2
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	0.1	8.1
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	0.0	2.7
Dendritic cells none	5.6	3.1	13.8	4.1	0.0	5.3
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.0	0.7
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.0	0.2
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	0.0	1.8
Macrophages rest	0.9	1.8	0.0	0.6	0.0	0.6
Macrophages LPS	7.5	4.0	0.0	5.4	0.1	6.3
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.0	0.3

HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.0	0.5
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.0	0.4
HUVEC IL-11	0.0	0.0	0.0	0.4	0.0	0.3
Lung Microvascular EC none	0.2	0.3	0.0	0.4	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	6.2	0.3	0.0	1.5
Astrocytes rest	67.8	97.3	100.0	100.0	12.0	100.0
Astrocytes TNFalpha + IL-1beta	100.0	100.0	74.2	97.3	100.0	74.7
KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.0	0.4
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0

CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.0	0.8
CCD1106 (Keratinocytes) TNFalpha + IL-1 beta	0.3	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	2.6	0.0	6.7
NCI-H292 none	0.3	0.3	0.0	1.7	0.0	0.6
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.0	0.5
NCI-H292 IL-9	0.3	0.0	0.0	0.7	0.0	0.5
NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.0	0.9
NCI-H292 IFN gamma	0.2	0.0	0.0	0.5	0.0	0.6
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	95.9	0.2	65.5
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	48.6	0.1	39.8
Lung fibroblast IL-4	26.1	28.7	19.1	27.4	0.1	21.2
Lung fibroblast IL-9	28.5	42.0	23.5	24.0	0.1	26.8
Lung fibroblast IL-13	31.6	14.6	4.5	11.9	0.0	10.4
Lung fibroblast IFN gamma	20.4	32.8	15.7	55.9	0.2	46.3
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.0	0.0	6.3
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	2.7	0.0	0.8
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	5.6	0.0	1.3
Dermal fibroblast IFN gamma	9.3	20.3	8.5	30.6	0.1	20.2
Dermal fibroblast IL-4	10.7	14.6	4.1	30.8	0.1	19.8
Dermal Fibroblasts rest	24.8	42.3	8.0	54.3	0.1	46.7

Neutrophils TNFa+LPS	0.7	0.0	0.0	0.9	0.0	0.4
Neutrophils rest	0.1	0.0	0.0	0.0	0.0	0.3
Colon	7.9	4.7	4.0	4.6	0.0	9.5
Lung	2.2	1.2	0.0	2.8	0.0	4.6
Thymus	3.1	0.8	0.0	0.0	0.0	0.4
Kidney	4.2	4.4	4.9	7.8	0.1	9.7

Table ATQ. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2

Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0 Summary: Ag4983/Ag6413/
Ag6428/Ag6430/Ag6431/Ag6440/Ag6442/Ag6446 Seven experiments with different probe
and primer sets are in excellent agreement. This panel confirms the expression of this gene
at low levels in the brains of an independent group of individuals. However, no differential
expression of this gene was detected between Alzheimer's diseased postmortem brains and
those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this
gene in treatment of central nervous system disorders.

Ag6424/ Ag6425 Expression of this gene is low/undetectable (CTs > 35) across all
of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this
gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of
expression of this gene is also seen in a number of cancer cell lines derived from gastric,
colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression
of this gene could be used as a marker to detect the presence of these cancers. Furthermore,
therapeutic modulation of the expression or function of this gene may be effective in the
treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous
cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at
moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal
muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity
of this gene may prove useful in the treatment of endocrine/metabolically related diseases,
such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as

5   Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be

10   used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for

15   further discussion on the utility of these genes.

General_screening_panel_v1.6 Summary: Ag6413/ Ag6424/Ag6425/ Ag6428/Ag6431/Ag6440/ Ag6446/Ag6964 Highest expression of this gene is detected in skeletal muscle, ovarian cancer IGROV-1 cell line, lung cancer LX-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in

20   panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Panel 4.1D Summary: Ag4983/Ag6413/Ag6425/Ag6428/Ag6431 Highest expression of this gene is detected in both resting and cytokine activated astrocytes

25   (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by

30   colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types

and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore,
5 antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

Ag6424/Ag6440 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two
10 experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived
15 from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney
20 cancers.

AU. CG56054-14: Integrin alpha 7-like protein.

Expression of gene CG56054-14 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6428, Ag6429, Ag6431, Ag6435, Ag6439, Ag6447, Ag6413 and Ag6964, described in Tables AUA, AUB, AUC, AUD, AUE, AUF, AUG, AUH, AUI and AUJ.
25 Results of the RTQ-PCR runs are shown in Tables AUK, AUL, AUM, AUN, AUO and AUP.

Table AUA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2342	633

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Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2364	634
Reverse	5'-aacagcagctctacctccagtt-3'	22	2398	635

Table AUB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2781	636
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2820	637
Reverse	5'-gcgcagtccagggtg-3'	15	2906	638

Table AUC. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	639
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	640
Reverse	5'-agggagtagccgaagctct-3'	19	1378	641

Table AUD. Probe Name Ag6429

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccgtgccccagtaccat-3'	17	3289	642
Probe	TET-5'-cgggcaccatcctgaggaacaac-3'-TAMRA	23	3355	643
Reverse	5'-gggcccagccaggat-3'	15	3391	644

5   Table AUE. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2900	645
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2941	646

| Reverse | 5'-ccgcgcggtcaaa-3' | 13 | 2967 | 647 |

Table AUF. Probe Name Ag6435

Primers	Sequences ·	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	648
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	649
Reverse	5'-cagggaccgggatga-3'	15	829	650

Table AUG. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	3157	651
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	3177	652
Reverse	5'-gaagaatcccatcttccacag-3'	21	3243	653

Table AUH. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	654
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	655
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	656

Table AUI. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	1980	657
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2031	658
Reverse	5'-gctgttgttccatccacatc-3'	20	2073	659

Table AUJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2986	660
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2957	661
Reverse	5'-gccaactgtgtggtgttca-3'	19	2931	662

Table AUK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6442, Run 264979298	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	23.7	24.8	18.0	18.8	17.1	21.6	19.2	18.8
AD 2 Hippo	41.2	52.9	32.3	28.7	27.9	28.9	49.7	10.4
AD 3 Hippo	8.9	6.4	3.7	7.5	4.8	6.1	20.4	0.0
AD 4 Hippo	14.8	25.5	10.7	18.8	18.3	17.6	5.6	4.6
AD 5 Hippo	44.8	41.8	53.2	38.4	46.7	42.6	57.4	11.0
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	100.0	90.1	100.0
Control 2 Hippo	24.3	36.1	18.7	29.5	8.5	32.5	28.5	3.1
Control 4 Hippo	42.9	43.8	27.0	32.3	29.9	37.9	86.5	43.8
Control (Path) 3 Hippo	14.2	11.4	4.6	6.0	5.2	6.4	0.0	5.3
AD 1 Temporal Ctx	23.3	15.9	12.9	17.1	12.8	24.5	16.8	9.0
AD 2 Temporal Ctx	41.5	47.3	31.0	39.8	45.1	27.5	21.6	21.0

AD 3 Temporal Ctx	9.5	9.8	6.0	11.3	4.1	9.0	5.7	3.9
AD 4 Temporal Ctx	30.6	39.0	20.2	25.3	6.8	30.4	8.7	7.7
AD 5 Inf Temporal Ctx	45.4	37.1	39.2	36.3	1.6	41.8	73.7	23.7
AD 5 Sup Temporal Ctx	51.1	39.0	42.0	32.3	33.2	38.7	55.9	11.4
AD 6 Inf Temporal Ctx	38.2	59.9	49.3	46.7	52.1	47.6	76.8	88.9
AD 6 Sup Temporal Ctx	43.8	48.6	48.3	50.3	37.6	50.3	59.9	61.1
Control 1 Temporal Ctx	12.2	23.0	12.9	15.6	6.7	24.0	46.7	2.8
Control 2 Temporal Ctx	14.2	32.5	18.2	17.4	7.3	14.9	50.0	16.0
Control 3 Temporal Ctx	15.1	15.3	9.6	14.5	4.4	16.5	9.5	3.1
Control 3 Temporal Ctx	23.7	25.0	15.2	13.1	11.7	23.8	13.6	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	27.0	30.6	24.8	39.8	46.0	13.8
Control (Path) 2 Temporal Ctx	24.5	25.9	16.0	20.4	9.8	24.8	0.0	2.6
Control (Path) 3 Temporal Ctx	11.7	16.0	7.5	10.9	3.5	11.9	31.0	6.3

Control (Path) 4 Temporal Ctx	21.9	27.4	17.1	18.2	14.8	21.6	39.5	7.0
AD 1 Occipital Ctx	16.0	11.9	10.2	11.5	15.0	16.0	6.3	0.0
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	10.7	6.0	6.4	8.8	8.0	10.2	4.9	0.0
AD 4 Occipital Ctx	18.9	23.7	13.0	17.9	6.8	18.6	11.1	3.5
AD 5 Occipital Ctx	24.8	28.3	25.3	22.5	12.7	22.7	42.3	3.8
AD 6 Occipital Ctx	20.6	31.9	20.2	17.0	5.9	22.1	14.8	8.5
Control 1 Occipital Ctx	9.5	14.4	6.0	8.7	4.1	7.2	8.8	1.3
Control 2 Occipital Ctx	31.9	42.6	26.4	33.2	20.3	29.3	82.4	13.7
Control 3 Occipital Ctx	18.8	13.0	10.7	17.1	7.5	19.2	8.8	5.0
Control 4 Occipital Ctx	18.2	17.0	12.0	12.6	3.3	13.6	24.0	1.3
Control (Path) 1 Occipital Ctx	38.2	52.5	35.6	36.1	25.9	39.5	100.0	12.1
Control (Path) 2 Occipital Ctx	9.6	14.1	6.7	7.9	7.4	7.0	9.3	13.2

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Control (Path) 3 Occipital Ctx	4.8	8.7	5.4	6.0	2.3	5.9	4.1	9.4
Control (Path) 4 Occipital Ctx	16.2	13.2	13.2	10.2	21.0	11.4	32.8	20.4
Control 1 Parietal Ctx	14.4	21.9	8.8	16.3	12.5	15.7	9.2	5.0
Control 2 Parietal Ctx	32.8	28.9	34.4	28.3	41.2	37.1	28.1	25.5
Control 3 Parietal Ctx	20.6	19.8	11.5	8.7	13.2	10.8	9.1	16.7
Control (Path) 1 Parietal Ctx	35.4	62.4	34.2	39.2	22.5	37.9	69.3	4.2
Control (Path) 2 Parietal Ctx	22.1	23.8	19.6	22.5	26.8	18.7	37.6	14.4
Control (Path) 3 Parietal Ctx	11.2	15.4	3.9	7.1	7.5	12.0	10.4	5.9
Control (Path) 4 Parietal Ctx	31.2	34.2	24.8	8.8	20.6	27.9	27.5	9.4

Table AUL. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1

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Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8
Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	100.0
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5

Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9
Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table AUM. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2

Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6

Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AUN. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	20.0	17.4	13.8	13.2	17.3	18.8
Melanoma* Hs688(A).T	0.5	2.0	0.8	0.9	0.9	0.4	0.7
Melanoma* Hs688(B).T	2.7	4.1	2.5	2.2	1.9	2.9	2.4
Melanoma* M14	0.3	0.7	0.4	0.4	0.0	0.4	0.7
Melanoma* LOXIMVI	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	15.2	30.4	18.2	14.6	4.4	18.3	15.9
Squamous cell carcinoma SCC-4	0.0	0.1	0.1	0.2	0.0	0.0	0.1
Testis Pool	5.2	8.8	10.4	9.0	10.0	9.1	9.9
Prostate ca.* (bone met) PC-3	1.9	2.5	1.9	1.8	1.8	1.3	4.3
Prostate Pool	8.1	11.5	11.3	12.1	10.0	28.5	10.0

Placenta	0.5	0.7	0.1	0.1	0.3	0.5	0.4
Uterus Pool	2.2	4.5	4.6	4.5	16.2	5.3	4.1
Ovarian ca. OVCAR-3	0.9	1.1	0.7	1.1	0.4	1.6	4.0
Ovarian ca. SK-OV-3	0.8	1.7	0.8	0.9	0.9	1.3	1.7
Ovarian ca. OVCAR-4	0.2	0.9	0.4	0.8	0.0	0.9	0.5
Ovarian ca. OVCAR-5	1.6	2.9	1.3	1.7	0.3	1.4	7.9
Ovarian ca. IGROV-1	100.0	77.9	84.7	97.9	27.0	69.3	75.8
Ovarian ca. OVCAR-8	13.6	14.0	15.6	14.6	7.6	17.3	16.7
Ovary	2.7	5.2	3.1	2.3	4.5	2.8	2.4
Breast ca. MCF-7	0.3	0.3	0.1	0.2	0.0	0.5	0.5
Breast ca. MDA-MB-231	0.1	0.4	0.2	0.2	0.0	0.2	0.3
Breast ca. BT 549	0.5	0.5	0.1	0.5	0.0	0.6	0.4
Breast ca. T47D	0.0	0.5	0.2	0.3	0.0	0.4	0.5
Breast ca. MDA-N	0.6	0.7	0.6	0.6	0.7	0.6	0.8
Breast Pool	15.0	21.8	14.6	10.7	42.9	12.2	16.7
Trachea	4.5	8.4	4.8	4.2	8.3	4.7	5.6
Lung	2.8	2.3	4.2	3.2	3.9	3.9	5.1
Fetal Lung	3.9	9.1	5.0	4.8	8.0	5.3	6.1
Lung ca. NCI-N417	2.0	3.5	3.3	2.6	0.2	4.0	2.3
Lung ca. LX-1	3.5	6.5	5.0	3.5	0.9	4.9	44.1
Lung ca. NCI-H146	0.1	0.3	0.1	0.2	0.0	0.1	0.1
Lung ca. SHP-77	4.0	6.8	5.3	4.5	0.2	4.5	3.8
Lung ca. A549	0.3	0.9	0.0	0.4	0.0	0.6	4.7

Lung ca. NCI-H526	0.2	0.9	0.6	0.3	0.0	0.4	0.5
Lung ca. NCI-H23	2.9	4.6	4.8	3.2	0.6	2.9	10.3
Lung ca. NCI-H460	0.0	0.2	0.1	0.3	0.0	0.0	0.3
Lung ca. HOP-62	0.5	0.5	1.0	0.6	0.0	0.5	0.7
Lung ca. NCI-H522	1.7	2.3	1.7	1.3	0.0	3.3	8.9
Liver	0.1	0.0	0.0	0.0	0.0	0.1	2.0
Fetal Liver	0.3	1.1	0.6	0.5	0.3	0.8	8.2
Liver ca. HepG2	0.1	0.2	0.0	0.2	0.0	0.1	2.4
Kidney Pool	27.9	47.0	33.9	28.1	100.0	43.2	32.8
Fetal Kidney	1.4	4.9	4.1	4.0	12.1	5.8	11.5
Renal ca. 786-0	0.2	0.2	0.3	0.1	0.0	0.3	0.9
Renal ca. A498	0.0	0.2	0.0	0.3	0.0	0.5	8.5
Renal ca. ACHN	1.5	2.5	1.7	1.5	0.0	1.2	2.5
Renal ca. UO-31	0.3	0.5	0.2	0.2	0.0	0.6	0.3
Renal ca. TK-10	1.9	3.1	2.0	1.9	0.7	2.1	4.6
Bladder	4.2	5.9	5.5	5.1	6.6	8.3	6.7
Gastric ca. (liver met.) NCI-N87	0.9	1.7	0.9	1.2	0.0	1.1	6.7
Gastric ca. KATO III	0.4	0.8	0.2	0.3	0.3	0.4	0.9
Colon ca. SW-948	0.0	0.2	0.2	0.2	0.0	0.3	1.2
Colon ca. SW480	20.9	41.8	27.0	23.3	4.4	23.0	33.7
Colon ca.* (SW480 met) SW620	13.3	16.4	12.8	10.3	1.7	6.1	25.0
Colon ca. HT29	0.2	0.0	0.2	0.2	0.0	0.0	0.3
Colon ca. HCT-116	2.1	3.2	2.5	2.0	0.5	2.1	4.3

Colon ca. CaCo-2	15.0	27.0	19.1	16.7	7.6	18.3	38.2
Colon cancer tissue	9.0	11.0	11.9	7.6	5.6	7.7	20.4
Colon ca. SW1116	1.3	2.5	2.0	1.5	1.1	1.8	6.0
Colon ca. Colo-205	0.1	0.3	0.2	0.0	0.0	0.2	0.8
Colon ca. SW-48	0.8	1.4	1.5	1.5	0.0	1.4	2.6
Colon Pool	20.3	28.1	23.2	18.7	44.8	25.5	20.6
Small Intestine Pool	14.0	17.1	11.2	13.0	26.8	12.8	10.4
Stomach Pool	8.1	14.3	9.5	9.3	24.0	8.5	10.7
Bone Marrow Pool	6.8	14.3	10.2	8.7	25.9	18.7	12.5
Fetal Heart	10.1	25.5	24.5	21.8	31.6	33.7	20.7
Heart Pool	28.7	29.7	25.9	17.2	23.5	33.7	26.1
Lymph Node Pool	17.6	33.7	22.1	23.7	64.6	19.9	24.7
Fetal Skeletal Muscle	31.9	54.3	48.6	46.3	46.7	19.1	50.7
Skeletal Muscle Pool	17.4	29.3	29.5	25.9	24.7	22.1	32.3
Spleen Pool	0.9	1.9	2.0	1.7	2.4	2.7	3.1
Thymus Pool	4.4	10.4	8.1	9.4	18.4	7.7	7.0
CNS cancer (glio/astro) U87-MG	9.8	14.9	10.7	10.0	5.8	10.9	14.1
CNS cancer (glio/astro) U-118-MG	3.5	4.7	3.8	3.1	1.5	3.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	2.6	2.1	1.0	0.7	1.4	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.1	0.2	0.2	0.1	0.1
CNS cancer (astro) SNB-75	8.1	14.9	6.5	10.0	3.1	11.7	9.7

CNS cancer (glio) SNB-19	79.6	100.0	100.0	100.0	12.8	100.0	100.0
CNS cancer (glio) SF-295	8.2	11.3	8.0	7.8	0.0	8.2	14.8
Brain (Amygdala) Pool	3.7	7.7	6.2	4.8	7.9	8.0	5.3
Brain (cerebellum)	12.0	19.8	10.7	9.7	1.8	8.8	9.7
Brain (fetal)	4.2	12.7	6.6	5.6	8.4	6.8	6.4
Brain (Hippocampus) Pool	7.5	11.7	8.6	6.9	9.9	11.0	10.2
Cerebral Cortex Pool	9.7	11.0	7.5	0.7	1.8	11.6	8.7
Brain (Substantia nigra) Pool	7.4	11.7	10.4	4.7	4.2	10.0	9.3
Brain (Thalamus) Pool	7.6	13.2	9.3	0.2	9.1	9.7	8.7
Brain (whole)	6.1	10.6	5.8	0.3	3.3	5.6	8.7
Spinal Cord Pool	10.1	14.7	11.0	7.6	13.1	12.2	9.0
Adrenal Gland	3.5	9.9	3.9	3.7	7.4	4.8	4.1
Pituitary gland Pool	0.9	1.1	1.2	1.1	1.8	1.4	0.5
Salivary Gland	0.9	1.8	1.3	0.9	2.3	1.1	1.0
Thyroid (female)	2.0	3.1	2.5	2.5	3.3	1.9	2.3
Pancreatic ca. CAPAN2	0.5	0.8	0.7	0.6	0.5	0.7	2.2
Pancreas Pool	1.2	2.0	1.1	1.6	3.5	3.2	2.3

Table AUO. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6439, Run 268760823	Rel. Exp.(%) Ag6447, Run 268761806

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Secondary Th1 act	0.1	0.3	1.3	0.7	0.0	0.0	0.0
Secondary Th2 act	0.5	0.3	1.2	0.8	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.7	0.0	0.0	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.7	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.4	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.3	0.4	0.7	0.0	0.0
Primary Tr1 act	0.1	0.0	0.7	0.7	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	0.1	0.3	0.0	1.2	0.0
Primary Th2 rest	0.0	0.0	0.4	0.2	0.0	0.0	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	5.4	2.4	0.8	2.6	0.0
CD45RO CD4 lymphocyte act	0.1	2.2	1.5	0.7	1.6	2.3	0.0
CD8 lymphocyte act	0.4	0.9	0.7	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	8.8	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.4	0.3	0.0	0.0	0.0
CD4 lymphocyte none	0.1	0.0	0.5	0.4	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	1.2	0.0
LAK cells rest	5.6	5.0	11.8	3.8	6.1	15.2	0.0
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0	0.0

LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	4.5	4.0	15.1	6.3	6.1	9.0	0.0
NK Cells IL-2 rest	0.9	0.1	3.4	2.5	0.0	1.4	0.0
Two Way MLR 3 day	1.4	1.1	2.2	1.3	0.9	1.4	0.0
Two Way MLR 5 day	4.5	0.9	0.8	0.9	0.0	0.0	0.0
Two Way MLR 7 day	2.3	0.7	1.1	2.6	2.9	3.7	0.0
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	1.3	0.0	0.0	0.0	0.0
PBMC PHA-L	0.3	0.2	0.6	0.7	0.0	0.0	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.7	0.2	0.0	0.0	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.9	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	29.1	8.1	0.0	68.8	0.0
EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	2.7	1.0	1.8	0.0
Dendritic cells none	5.6	3.1	4.1	5.3	0.7	0.0	0.0
Dendritic cells LPS	1.6	0.3	1.0	0.7	0.0	0.0	0.0
Dendritic cells anti-CD40	2.0	1.6	0.5	0.2	1.6	0.0	0.0
Monocytes rest	0.2	0.0	0.4	0.0	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	5.7	1.8	0.0	2.6	0.4
Macrophages rest	0.9	1.8	0.6	0.6	0.0	0.0	0.0

Macrophages LPS	7.5	4.0	5.4	6.3	0.8	9.2	0.0
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.3	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.5	0.0	0.0	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.6	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.4	0.3	0.0	0.0	0.0
Lung Microvascular EC none	0.2	0.3	0.4	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.5	0.0	0.3
Coronery artery SMC TNFalpha + IL-1beta	0.4	0.9	0.3	1.5	0.0	0.0	0.0
Astrocytes rest	67.8	97.3	100.0	100.0	100.0	100.0	54.3

Astrocytes TNFalpha + IL-1 beta	100.0	100.0	97.3	74.7	97.9	95.9	100.0
KU-812 (Basophil) rest	0.1	0.0	0.0	0.4	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.8	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	2.6	6.7	5.1	8.5	0.6
NCI-H292 none	0.3	0.3	1.7	0.6	0.0	0.0	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.5	0.0	0.0	0.0
NCI-H292 IL-9	0.3	0.0	0.7	0.5	0.0	0.0	0.0
NCI-H292 IL-13	0.6	0.6	0.9	0.9	0.0	0.0	0.0
NCI-H292 IFN gamma	0.2	0.0	0.5	0.6	0.0	0.0	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	95.9	65.5	62.9	94.0	26.2
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	48.6	39.8	25.2	62.9	28.3
Lung fibroblast IL-4	26.1	28.7	27.4	21.2	23.3	34.9	16.0
Lung fibroblast IL-9	28.5	42.0	24.0	26.8	20.4	96.6	9.3
Lung fibroblast IL-13	31.6	14.6	11.9	10.4	15.0	13.4	4.3
Lung fibroblast IFN gamma	20.4	32.8	55.9	46.3	29.9	89.5	25.2

Dermal fibroblast CCD1070 rest	2.5	2.9	6.0	6.3	5.6	4.1	0.0
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	2.7	0.8	0.8	2.3	1.1
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	5.6	1.3	0.7	0.0	1.6
Dermal fibroblast IFN gamma	9.3	20.3	30.6	20.2	20.0	26.6	4.9
Dermal fibroblast IL-4	10.7	14.6	30.8	19.8	22.7	25.5	13.5
Dermal Fibroblasts rest	24.8	42.3	54.3	46.7	20.7	47.3	15.8
Neutrophils TNFa+LPS	0.7	0.0	0.9	0.4	1.2	0.0	0.0
Neutrophils rest	0.1	0.0	0.0	0.3	0.0	0.0	0.0
Colon	7.9	4.7	4.6	9.5	7.9	8.4	4.8
Lung	2.2	1.2	2.8	4.6	1.6	2.1	0.0
Thymus	3.1	0.8	0.0	0.4	2.0	2.4	0.0
Kidney	4.2	4.4	7.8	9.7	10.2	5.2	0.6

Table AUP. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	**100.0**	**100.0**	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9

Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2
Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0 Summary: Ag4983/Ag6413/Ag6428/Ag6431/ Ag6435/Ag6439/Ag6442/ Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6429 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of expression of this gene is also seen in a number of cancer cell lines derived from gastric,

colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous

5   cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases,

10   such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as

15   Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be

20   used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for

25   further discussion on the utility of these genes.

General_screening_panel_v1.6 Summary: Ag6413/Ag6428/Ag6431/ Ag6435/Ag6439 Six experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-28.5). In addition, consistent with

30   expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen

in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6429/Ag6447 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

5   **Panel 4.1D**

Summary: Ag4983/Ag6413/Ag6428/Ag6431/Ag6435/Ag6439/Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics

10   with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a

15   functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore,

20   antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in

25   normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding

30   normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this

gene may be useful in the treatment of melanoma, colon, lung. bladder, prostate and kidney cancers.

AV. CG56054-15: Integrin alpha 7-like protein.

Expression of gene CG56054-15 was assessed using the primer-probe sets Ag6425, Ag6428, Ag6432, Ag6435 and Ag6447, described in Tables AVA, AVB, AVC, AVD and AVE. Results of the RTQ-PCR runs are shown in Tables AVF, AVG and AVH.

Table AVA. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	1888	663
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	1920	664
Reverse	5'-gccctggatgcccat-3'	15	1939	665

Table AVB. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	666
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	667
Reverse	5'-agggagtagccgaagctct-3'	19	1378	668

Table AVC. Probe Name Ag6432

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gaccttgtcctacagtctccagac-3'	24	1841	669
Probe	TET-5'-tgcacacccatcctggctgct-3'-TAMRA	22	1892	670
Reverse	5'-gctcgggatgcccgt-3'	15	1915	671

Table AVD. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	672

| Probe | TET-5'-acctggcacacctggacgacg-3'-TAMRA | 21 | 766 | 673 |
| Reverse | 5'-cagggaccgggatga-3' | 15 | 829 | 674 |

Table AVE. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	675
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	676
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	677

Table AVF. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	18.0	17.1	18.8
AD 2 Hippo	32.3	27.9	10.4
AD 3 Hippo	3.7	4.8	0.0
AD 4 Hippo	10.7	18.3	4.6
AD 5 Hippo	53.2	46.7	11.0
AD 6 Hippo	100.0	100.0	100.0
Control 2 Hippo	18.7	8.5	3.1
Control 4 Hippo	27.0	29.9	43.8
Control (Path) 3 Hippo	4.6	5.2	5.3
AD 1 Temporal Ctx	12.9	12.8	9.0
AD 2 Temporal Ctx	31.0	45.1	21.0
AD 3 Temporal Ctx	6.0	4.1	3.9
AD 4 Temporal Ctx	20.2	6.8	7.7
AD 5 Inf Temporal Ctx	39.2	1.6	23.7
AD 5 Sup Temporal Ctx	42.0	33.2	11.4

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AD 6 Inf Temporal Ctx	49.3	52.1	88.9
AD 6 Sup Temporal Ctx	48.3	37.6	61.1
Control 1 Temporal Ctx	12.9	6.7	2.8
Control 2 Temporal Ctx	18.2	7.3	16.0
Control 3 Temporal Ctx	9.6	4.4	3.1
Control 3 Temporal Ctx	15.2	11.7	13.6
Control (Path) 1 Temporal Ctx	27.0	24.8	13.8
Control (Path) 2 Temporal Ctx	16.0	9.8	2.6
Control (Path) 3 Temporal Ctx	7.5	3.5	6.3
Control (Path) 4 Temporal Ctx	17.1	14.8	7.0
AD 1 Occipital Ctx	10.2	15.0	0.0
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 3 Occipital Ctx	6.4	8.0	0.0
AD 4 Occipital Ctx	13.0	6.8	3.5
AD 5 Occipital Ctx	25.3	12.7	3.8
AD 6 Occipital Ctx	20.2	5.9	8.5
Control 1 Occipital Ctx	6.0	4.1	1.3
Control 2 Occipital Ctx	26.4	20.3	13.7
Control 3 Occipital Ctx	10.7	7.5	5.0
Control 4 Occipital Ctx	12.0	3.3	1.3
Control (Path) 1 Occipital Ctx	35.6	25.9	12.1
Control (Path) 2 Occipital Ctx	6.7	7.4	13.2
Control (Path) 3 Occipital Ctx	5.4	2.3	9.4

Control (Path) 4 Occipital Ctx	13.2	21.0	20.4
Control 1 Parietal Ctx	8.8	12.5	5.0
Control 2 Parietal Ctx	34.4	41.2	25.5
Control 3 Parietal Ctx	11.5	13.2	16.7
Control (Path) 1 Parietal Ctx	34.2	22.5	4.2
Control (Path) 2 Parietal Ctx	19.6	26.8	14.4
Control (Path) 3 Parietal Ctx	3.9	7.5	5.9
Control (Path) 4 Parietal Ctx	24.8	20.6	9.4

Table AVG. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6435, Run 277223167	Tissue Name	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6435, Run 277223167
Adipose	2.6	20.0	13.2	Renal ca. TK-10	0.4	3.1	0.7
Melanoma* Hs688(A).T	0.0	2.0	0.9	Bladder	0.0	5.9	6.6
Melanoma* Hs688(B).T	0.2	4.1	1.9	Gastric ca. (liver met.) NCI-N87	0.0	1.7	0.0
Melanoma* M14	0.0	0.7	0.0	Gastric ca. KATO III	0.5	0.8	0.3
Melanoma* LOXIMVI	0.0	0.1	0.0	Colon ca. SW-948	1.5	0.2	0.0
Melanoma* SK-MEL-5	2.2	30.4	4.4	Colon ca. SW480	5.2	41.8	4.4
Squamous cell carcinoma SCC-4	0.0	0.1	0.0	Colon ca.* (SW480 met) SW620	4.8	16.4	1.7
Testis Pool	3.5	8.8	10.0	Colon ca. HT29	0.0	0.0	0.0

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Prostate ca.* (bone met) PC-3	0.5	2.5	1.8	Colon ca. HCT-116	0.2	3.2	0.5
Prostate Pool	1.0	11.5	10.0	Colon ca. CaCo-2	3.6	27.0	7.6
Placenta	0.0	0.7	0.3	Colon cancer tissue	3.3	11.0	5.6
Uterus Pool	1.5	4.5	16.2	Colon ca. SW1116	3.0	2.5	1.1
Ovarian ca. OVCAR-3	0.3	1.1	0.4	Colon ca. Colo-205	0.4	0.3	0.0
Ovarian ca. SK-OV-3	0.2	1.7	0.9	Colon ca. SW-48	3.6	1.4	0.0
Ovarian ca. OVCAR-4	0.0	0.9	0.0	Colon Pool	5.0	28.1	44.8
Ovarian ca. OVCAR-5	1.3	2.9	0.3	Small Intestine Pool	1.7	17.1	26.8
Ovarian ca. IGROV-1	**100.0**	77.9	27.0	Stomach Pool	2.3	14.3	24.0
Ovarian ca. OVCAR-8	21.9	14.0	7.6	Bone Marrow Pool	1.6	14.3	25.9
Ovary	0.3	5.2	4.5	Fetal Heart	2.3	25.5	31.6
Breast ca. MCF-7	0.0	0.3	0.0	Heart Pool	7.0	29.7	23.5
Breast ca. MDA-MB-231	0.0	0.4	0.0	Lymph Node Pool	6.1	33.7	64.6
Breast ca. BT 549	0.0	0.5	0.0	Fetal Skeletal Muscle	5.2	54.3	46.7
Breast ca. T47D	0.0	0.5	0.0	Skeletal Muscle Pool	9.2	29.3	24.7
Breast ca. MDA-N	0.0	0.7	0.7	Spleen Pool	0.0	1.9	2.4
Breast Pool	4.1	21.8	42.9	Thymus Pool	2.0	10.4	18.4
Trachea	0.7	8.4	8.3	CNS cancer (glio/astro) U87-MG	1.5	14.9	5.8
Lung	0.7	2.3	3.9	CNS cancer (glio/astro) U-118-MG	0.3	4.7	1.5

Fetal Lung	0.3	9.1	8.0	CNS cancer (neuro;met) SK-N-AS	0.0	2.6	0.7
Lung ca. NCI-N417	0.9	3.5	0.2	CNS cancer (astro) SF-539	0.0	0.0	0.2
Lung ca. LX-1	2.7	6.5	0.9	CNS cancer (astro) SNB-75	1.1	14.9	3.1
Lung ca. NCI-H146	0.0	0.3	0.0	CNS cancer (glio) SNB-19	79.0	100.0	12.8
Lung ca. SHP-77	0.4	6.8	0.2	CNS cancer (glio) SF-295	0.0	11.3	0.0
Lung ca. A549	2.6	0.9	0.0	Brain (Amygdala) Pool	0.8	7.7	7.9
Lung ca. NCI-H526	0.0	0.9	0.0	Brain (cerebellum)	0.4	19.8	1.8
Lung ca. NCI-H23	1.0	4.6	0.6	Brain (fetal)	0.7	12.7	8.4
Lung ca. NCI-H460	0.0	0.2	0.0	Brain (Hippocampus) Pool	3.2	11.7	9.9
Lung ca. HOP-62	0.0	0.5	0.0	Cerebral Cortex Pool	0.6	11.0	1.8
Lung ca. NCI-H522	0.6	2.3	0.0	Brain (Substantia nigra) Pool	2.2	11.7	4.2
Liver	0.0	0.0	0.0	Brain (Thalamus) Pool	2.7	13.2	9.1
Fetal Liver	0.3	1.1	0.3	Brain (whole)	0.4	10.6	3.3
Liver ca. HepG2	0.3	0.2	0.0	Spinal Cord Pool	2.3	14.7	13.1
Kidney Pool	0.0	47.0	100.0	Adrenal Gland	0.3	9.9	7.4
Fetal Kidney	0.0	4.9	12.1	Pituitary gland Pool	0.0	1.1	1.8
Renal ca. 786-0	0.0	0.2	0.0	Salivary Gland	0.0	1.8	2.3
Renal ca. A498	1.8	0.2	0.0	Thyroid (female)	0.3	3.1	3.3

| Renal ca. ACHN | 0.5 | 2.5 | 0.0 | Pancreatic ca. CAPAN2 | 0.0 | 0.8 | 0.5 |
| Renal ca. UO-31 | 0.0 | 0.5 | 0.0 | Pancreas Pool | 0.0 | 2.0 | 3.5 |

Table AVH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.0	1.3	0.0	0.0
Secondary Th2 act	0.0	1.2	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.0	0.7	0.0
Secondary Tr1 rest	0.0	0.4	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0
Primary Th2 act	0.0	0.3	0.7	0.0
Primary Tr1 act	0.0	0.7	0.0	0.0
Primary Th1 rest	0.0	0.1	0.0	0.0
Primary Th2 rest	0.0	0.4	0.0	0.0
Primary Tr1 rest	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	5.4	0.8	0.0
CD45RO CD4 lymphocyte act	0.0	1.5	1.6	0.0
CD8 lymphocyte act	0.0	0.7	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	8.8	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.4	0.0	0.0
CD4 lymphocyte none	0.0	0.5	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	0.0	0.0
LAK cells rest	2.7	11.8	6.1	0.0

LAK cells IL-2	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	15.1	6.1	0.0
NK Cells IL-2 rest	0.0	3.4	0.0	0.0
Two Way MLR 3 day	0.0	2.2	0.9	0.0
Two Way MLR 5 day	0.0	0.8	0.0	0.0
Two Way MLR 7 day	13.2	1.1	2.9	0.0
PBMC rest	0.0	0.0	0.0	0.0
PBMC PWM	0.0	1.3	0.0	0.0
PBMC PHA-L	0.0	0.6	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.7	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.9	0.0	0.0
EOL-1 dbcAMP	9.1	29.1	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	1.0	0.0
Dendritic cells none	13.8	4.1	0.7	0.0
Dendritic cells LPS	0.0	1.0	0.0	0.0
Dendritic cells anti-CD40	3.3	0.5	1.6	0.0
Monocytes rest	0.0	0.4	0.0	0.0
Monocytes LPS	0.0	5.7	0.0	0.4
Macrophages rest	0.0	0.6	0.0	0.0
Macrophages LPS	0.0	5.4	0.8	0.0
HUVEC none	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0	0.0

HUVEC TNF alpha + IFN gamma	0.0	0.0	0.6	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0	0.0
HUVEC IL-11	0.0	0.4	0.0	0.0
Lung Microvascular EC none	0.0	0.4	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.0	0.5	0.3
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.3	0.0	0.0
Astrocytes rest	100.0	100.0	100.0	54.3
Astrocytes TNFalpha + IL-1beta	74.2	97.3	97.9	100.0
KU-812 (Basophil) rest	0.0	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Liver cirrhosis	4.6	2.6	5.1	0.6
NCI-H292 none	0.0	1.7	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.7	0.0	0.0
NCI-H292 IL-13	0.0	0.9	0.0	0.0

NCI-H292 IFN gamma	0.0	0.5	0.0	0.0
HPAEC none	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0	0.0
Lung fibroblast none	31.4	95.9	62.9	26.2
Lung fibroblast TNF alpha + IL-1 beta	22.2	48.6	25.2	28.3
Lung fibroblast IL-4	19.1	27.4	23.3	16.0
Lung fibroblast IL-9	23.5	24.0	20.4	9.3
Lung fibroblast IL-13	4.5	11.9	15.0	4.3
Lung fibroblast IFN gamma	15.7	55.9	29.9	25.2
Dermal fibroblast CCD1070 rest	0.0	6.0	5.6	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	2.7	0.8	1.1
Dermal fibroblast CCD1070 IL-1 beta	0.0	5.6	0.7	1.6
Dermal fibroblast IFN gamma	8.5	30.6	20.0	4.9
Dermal fibroblast IL-4	4.1	30.8	22.7	13.5
Dermal Fibroblasts rest	8.0	54.3	20.7	15.8
Neutrophils TNFa+LPS	0.0	0.9	1.2	0.0
Neutrophils rest	0.0	0.0	0.0	0.0
Colon	4.0	4.6	7.9	4.8
Lung	0.0	2.8	1.6	0.0
Thymus	0.0	0.0	2.0	0.0
Kidney	4.9	7.8	10.2	0.6

CNS_neurodegeneration_v1.0 Summary: Ag6428/Ag6435/Ag6447 Three experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this

experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6432, Ag6425 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

5   General_screening_panel_v1.6 Summary: Ag6425// Ag6428/Ag6435 Four experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in kidney, a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-30). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of

10   central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6432/Ag6447 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag6425/ Ag6428/Ag6435/Ag6447 Four experiments with

15   different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=31-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

20   In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and

25   inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Ag6432 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

AW. CG56054-16: Integrin alpha 7-like protein.

Expression of gene CG56054-16 was assessed using the primer-probe sets Ag6427, Ag6434, Ag6435 and Ag6447, described in Tables AWA, AWB, AWC and AWD. Results of the RTQ-PCR runs are shown in Tables AWE, AWF and AWG.

Table AWA. Probe Name Ag6427

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	678
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	679
Reverse	5'-ccctggatgcccatc-3'	15	1391	680

5   Table AWB. Probe Name Ag6434

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctttgatggtgatgggaa-3'	19	1279	681
Probe	TET-5'-cttcatctaccatgggagcagcctg-3'-TAMRA	25	1301	682
Reverse	5'-gctcgggatgcccac-3'	15	1368	683

Table AWC. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	684
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	685
Reverse	5'-cagggaccgggatga-3'	15	829	686

Table AWD. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	687
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	688
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	689

Table AWE. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6434, Run 269253996	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6447, Run 269254007	Tissue Name	Rel. Exp.(%) Ag6434, Run 269253996	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	17.3	17.1	18.8	Control (Path) 3 Temporal Ctx	9.2	3.5	6.3
AD 2 Hippo	33.0	27.9	10.4	Control (Path) 4 Temporal Ctx	13.8	14.8	7.0
AD 3 Hippo	3.4	4.8	0.0	AD 1 Occipital Ctx	8.4	15.0	0.0
AD 4 Hippo	9.0	18.3	4.6	AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 5 hippo	66.4	46.7	11.0	AD 3 Occipital Ctx	3.8	8.0	0.0
AD 6 Hippo	100.0	100.0	100.0	AD 4 Occipital Ctx	1.4	6.8	3.5
Control 2 Hippo	23.3	8.5	3.1	AD 5 Occipital Ctx	21.3	12.7	3.8
Control 4 Hippo	26.6	29.9	43.8	AD 6 Occipital Ctx	15.5	5.9	8.5
Control (Path) 3 Hippo	7.0	5.2	5.3	Control 1 Occipital Ctx	5.5	4.1	1.3
AD 1 Temporal Ctx	13.7	12.8	9.0	Control 2 Occipital Ctx	33.7	20.3	13.7
AD 2 Temporal Ctx	35.8	45.1	21.0	Control 3 Occipital Ctx	3.0	7.5	5.0
AD 3 Temporal Ctx	7.2	4.1	3.9	Control 4 Occipital Ctx	8.1	3.3	1.3

AD 4 Temporal Ctx	6.7	6.8	7.7	Control (Path) 1 Occipital Ctx	39.0	25.9	12.1
AD 5 Inf Temporal Ctx	21.9	1.6	23.7	Control (Path) 2 Occipital Ctx	4.2	7.4	13.2
AD 5 SupTemporal Ctx	31.6	33.2	11.4	Control (Path) 3 Occipital Ctx	3.2	2.3	9.4
AD 6 Inf Temporal Ctx	52.9	52.1	88.9	Control (Path) 4 Occipital Ctx	9.3	21.0	20.4
AD 6 Sup Temporal Ctx	71.2	37.6	61.1	Control 1 Parietal Ctx	10.1	12.5	5.0
Control 1 Temporal Ctx	10.3	6.7	2.8	Control 2 Parietal Ctx	43.5	41.2	25.5
Control 2 Temporal Ctx	16.2	7.3	16.0	Control 3 Parietal Ctx	15.9	13.2	16.7
Control 3 Temporal Ctx	8.5	4.4	3.1	Control (Path) 1 Parietal Ctx	24.8	22.5	4.2
Control 4 Temporal Ctx	13.6	11.7	13.6	Control (Path) 2 Parietal Ctx	22.1	26.8	14.4
Control (Path) 1 Temporal Ctx	29.9	24.8	13.8	Control (Path) 3 Parietal Ctx	9.3	7.5	5.9
Control (Path) 2 Temporal Ctx	13.2	9.8	2.6	Control (Path) 4 Parietal Ctx	34.6	20.6	9.4

Table AWF. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6434, Run 277222451	Rel. Exp.(%) Ag6435, Run 277223167	Tissue Name	Rel. Exp.(%) Ag6434, Run 277222451	Rel. Exp.(%) Ag6435, Run 277223167
Adipose	9.5	13.2	Renal ca. TK-10	3.0	0.7

Melanoma* Hs688(A).T	0.9	0.9	Bladder	3.4	6.6
Melanoma* Hs688(B).T	3.7	1.9	Gastric ca. (liver met.) NCI-N87	1.1	0.0
Melanoma* M14	0.7	0.0	Gastric ca. KATO III	0.0	0.3
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW-948	0.0	0.0
Melanoma* SK-MEL-5	14.7	4.4	Colon ca. SW480	28.3	4.4
Squamous cell carcinoma SCC-4	0.0	0.0	Colon ca.* (SW480 met) SW620	11.7	1.7
Testis Pool	5.7	10.0	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	1.5	1.8	Colon ca. HCT-116	5.0	0.5
Prostate Pool	4.2	10.0	Colon ca. CaCo-2	14.9	7.6
Placenta	0.5	0.3	Colon cancer tissue	9.2	5.6
Uterus Pool	2.5	16.2	Colon ca. SW1116	2.2	1.1
Ovarian ca. OVCAR-3	0.8	0.4	Colon ca. Colo-205	0.0	0.0
Ovarian ca. SK-OV-3	0.8	0.9	Colon ca. SW-48	1.4	0.0
Ovarian ca. OVCAR-4	0.5	0.0	Colon Pool	14.2	44.8
Ovarian ca. OVCAR-5	2.9	0.3	Small Intestine Pool	7.4	26.8
Ovarian ca. IGROV-1	73.7	27.0	Stomach Pool	9.2	24.0
Ovarian ca. OVCAR-8	20.7	7.6	Bone Marrow Pool	4.6	25.9
Ovary	4.0	4.5	Fetal Heart	11.3	31.6
Breast ca. MCF-7	0.5	0.0	Heart Pool	15.2	23.5
Breast ca. MDA-MB-231	0.5	0.0	Lymph Node Pool	14.1	64.6
Breast ca. BT 549	0.5	0.0	Fetal Skeletal Muscle	33.0	46.7
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	21.2	24.7

Breast ca. MDA-N	0.0	0.7	Spleen Pool	1.2	2.4
Breast Pool	9.6	42.9	Thymus Pool	6.1	18.4
Trachea	5.3	8.3	CNS cancer (glio/astro) U87-MG	10.4	5.8
Lung	1.3	3.9	CNS cancer (glio/astro) U-118-MG	3.4	1.5
Fetal Lung	5.0	8.0	CNS cancer (neuro;met) SK-N-AS	1.8	0.7
Lung ca. NCI-N417	3.0	0.2	CNS cancer (astro) SF-539	0.0	0.2
Lung ca. LX-1	4.3	0.9	CNS cancer (astro) SNB-75	12.0	3.1
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	100.0	12.8
Lung ca. SHP-77	4.9	0.2	CNS cancer (glio) SF-295	7.7	0.0
Lung ca. A549	0.7	0.0	Brain (Amygdala) Pool	5.5	7.9
Lung ca. NCI-H526	0.0	0.0	Brain (cerebellum)	11.0	1.8
Lung ca. NCI-H23	3.1	0.6	Brain (fetal)	6.9	8.4
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	8.5	9.9
Lung ca. HOP-62	0.0	0.0	Cerebral Cortex Pool	6.8	1.8
Lung ca. NCI-H522	1.4	0.0	Brain (Substantia nigra) Pool	5.2	4.2
Liver	0.0	0.0	Brain (Thalamus) Pool	6.8	9.1
Fetal Liver	0.5	0.3	Brain (whole)	6.8	3.3
Liver ca. HepG2	0.5	0.0	Spinal Cord Pool	6.4	13.1
Kidney Pool	22.8	100.0	Adrenal Gland	8.4	7.4
Fetal Kidney	2.4	12.1	Pituitary gland Pool	0.6	1.8
Renal ca. 786-0	0.0	0.0	Salivary Gland	1.6	2.3

Renal ca. A498	0.0	0.0	Thyroid (female)	2.6	3.3
Renal ca. ACHN	0.7	0.0	Pancreatic ca. CAPAN2	0.9	0.5
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.8	3.5

Table AWG. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6434, Run 268713326	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6447, Run 268761806	Tissue Name	Rel. Exp.(%) Ag6434, Run 268713326	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.0	0.0	0.0	HUVEC IL-1beta	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0	HUVEC IFN gamma	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.6	0.0
Secondary Th1 rest	0.0	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.7	0.0	HUVEC IL-11	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.0	0.0	Lung Microvascular EC none	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0
Primary Th2 act	0.0	0.7	0.0	Microvascular Dermal EC none	0.0	0.0	0.0
Primary Tr1 act	0.0	0.0	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0
Primary Th2 rest	0.0	0.0	0.0	Small airway epithelium none	0.0	0.0	0.0

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Primary Tr1 rest	0.0	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.8	0.0	Coronery artery SMC rest	0.0	0.5	0.3
CD45RO CD4 lymphocyte act	3.9	1.6	0.0	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0	0.0
CD8 lymphocyte act	0.0	0.0	0.0	Astrocytes rest	100.0	100.0	54.3
Secondary CD8 lymphocyte rest	0.0	0.0	0.0	Astrocytes TNFalpha + IL-1beta	97.3	97.9	100.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0	KU-812 (Basophil) rest	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0	KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	0.0	CCD1106 (Keratinocytes) none	0.0	0.0	0.0
LAK cells rest	7.9	6.1	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0
LAK cells IL-2	0.0	0.0	0.0	Liver cirrhosis	3.4	5.1	0.6
LAK cells IL-2+IL-12	0.0	0.0	0.0	NCI-H292 none	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0	NCI-H292 IL-4	0.0	0.0	0.0
LAK cells IL-2+IL-18	0.0	0.0	0.0	NCI-H292 IL-9	0.0	0.0	0.0
LAK cells PMA/ionomycin	7.0	6.1	0.0	NCI-H292 IL-13	0.0	0.0	0.0
NK Cells IL-2 rest	0.0	0.0	0.0	NCI-H292 IFN gamma	0.0	0.0	0.0
Two Way MLR 3 day	0.0	0.9	0.0	HPAEC none	0.0	0.0	0.0
Two Way MLR 5 day	0.0	0.0	0.0	HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0

Two Way MLR 7 day	0.0	2.9	0.0	Lung fibroblast none	72.7	62.9	26.2
PBMC rest	0.0	0.0	0.0	Lung fibroblast TNF alpha + IL-1 beta	36.6	25.2	28.3
PBMC PWM	0.0	0.0	0.0	Lung fibroblast IL-4	62.4	23.3	16.0
PBMC PHA-L	0.0	0.0	0.0	Lung fibroblast IL-9	52.5	20.4	9.3
Ramos (B cell) none	0.0	0.0	0.0	Lung fibroblast IL-13	14.6	15.0	4.3
Ramos (B cell) ionomycin	0.0	0.0	0.0	Lung fibroblast IFN gamma	41.5	29.9	25.2
B lymphocytes PWM	0.0	0.0	0.0	Dermal fibroblast CCD1070 rest	5.1	5.6	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	7.2	0.8	1.1
EOL-1 dbcAMP	4.4	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.7	1.6
EOL-1 dbcAMP PMA/ionomycin	0.0	1.0	0.0	Dermal fibroblast IFN gamma	24.5	20.0	4.9
Dendritic cells none	4.5	0.7	0.0	Dermal fibroblast IL-4	28.7	22.7	13.5
Dendritic cells LPS	0.0	0.0	0.0	Dermal Fibroblasts rest	44.4	20.7	15.8
Dendritic cells anti-CD40	0.0	1.6	0.0	Neutrophils TNFa+LPS	0.0	1.2	0.0
Monocytes rest	0.0	0.0	0.0	Neutrophils rest	0.0	0.0	0.0
Monocytes LPS	5.9	0.0	0.4	Colon	4.1	7.9	4.8
Macrophages rest	0.0	0.0	0.0	Lung	0.0	1.6	0.0
Macrophages LPS	9.1	0.8	0.0	Thymus	0.0	2.0	0.0
HUVEC none	0.0	0.0	0.0	Kidney	8.1	10.2	0.6
HUVEC starved	0.0	0.0	0.0				

CNS_neurodegeneration_v1.0 Summary: Ag6434/Ag6435/Ag6447 Three experiments with different probe and primer sets are in good agreements. This panel

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confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous

5   system disorders.

Ag6427 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.6 Summary: Ag6434 Highest expression of this gene is detected in a brain cancer SNB-19 cell lines (CT=31.9). In addition, moderate to low

10   levels of expression of this gene is also seen in some of the colon, ovarian and brain cancer cell lines. Thus, expression of this gene may be used as a marker to detect the presence of colon, ovarian and brain cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of these cancers.

Ag6435 Highest expression of this gene is detected in kidney (CT=30.6). Moderate

15   levels of expression of this gene is seen in normal tissues represented by breast, testis, prostate, uterus, gastrointestinal tract, and tissues with metabolic/endocrine functions including adipose, heart, skeletal muscle, and adernal gland. Therefore, therapeutic modulation of this gene or its protein product may be useful in the treatment of diseases associated with these tissues, including obesity, diabetes and inflammatory bowel disease.

20   In addition, moderate to low levels of expression of this gene is also seen in some regions of central nervous system, and some brain, colon and ovarian cancer cell lines.

Ag6427/Ag6447 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag6434/Ag6435/Ag6447 Three experiments with different

25   probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=31-34.8). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting

30   and cytokine treated lung and dermal fibroblasts. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these

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cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Ag6427 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

AX. CG56054-17: Integrin alpha 7-like protein.

Expression of gene CG56054-17 was assessed using the primer-probe sets Ag6425, Ag6426, Ag6435, Ag6439, Ag6440 and Ag6447, described in Tables AXA, AXB, AXC, AXD, AXE and AXF. Results of the RTQ-PCR runs are shown in Tables AXG, AXH and AXI.

Table AXA. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	1499	690
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	1531	691
Reverse	5'-gccctggatgcccat-3'	15	1550	692

Table AXB. Probe Name Ag6426

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtcactgggctgggatct-3'	18	1156	693
Probe	TET-5'-ctctccggctctgcggctc-3'-TAMRA	19	1177	694
Reverse	5'-actccttctgccaccaca-3'	18	1254	695

Table AXC. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	696
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	697
Reverse	5'-cagggaccgggatga-3'	15	829	698

Table AXD. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	1253	699
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	1273	700
Reverse	5'-gaagaatcccatcttccacag-3'	21	1339	701

Table AXE. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	1456	702
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	1523	703
Reverse	5'-ccctggatgcccatc-3'	15	1549	704

Table AXF. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	705
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	706
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	707

Table AXG. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6425, Run 266937076	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	24.1	17.1	21.6	18.9	18.8
AD 2 Hippo	48.0	27.9	28.9	61.1	10.4
AD 3 Hippo	6.5	4.8	6.1	9.7	0.0
AD 4 Hippo	13.8	18.3	17.6	23.3	4.6
AD 5 Hippo	52.9	46.7	42.6	34.6	11.0
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0

Control 2 Hippo	10.6	8.5	32.5	29.9	3.1
Control 4 Hippo	51.8	29.9	37.9	54.7	43.8
Control (Path) 3 Hippo	9.8	5.2	6.4	5.8	5.3
AD 1 Temporal Ctx	10.1	12.8	24.5	12.6	9.0
AD 2 Temporal Ctx	33.7	45.1	27.5	59.0	21.0
AD 3 Temporal Ctx	0.0	4.1	9.0	17.1	3.9
AD 4 Temporal Ctx	12.8	6.8	30.4	29.9	7.7
AD 5 Inf Temporal Ctx	59.0	1.6	41.8	41.8	23.7
AD 5 Sup Temporal Ctx	21.9	33.2	38.7	39.2	11.4
AD 6 Inf Temporal Ctx	73.7	52.1	47.6	48.6	88.9
AD 6 Sup Temporal Ctx	50.3	37.6	50.3	17.0	61.1
Control 1 Temporal Ctx	11.9	6.7	24.0	23.3	2.8
Control 2 Temporal Ctx	18.6	7.3	14.9	43.5	16.0
Control 3 Temporal Ctx	6.0	4.4	16.5	9.2	3.1
Control 3 Temporal Ctx	25.7	11.7	23.8	30.1	13.6
Control (Path) 1 Temporal Ctx	18.0	24.8	39.8	51.1	13.8
Control (Path) 2 Temporal Ctx	18.4	9.8	24.8	7.2	2.6
Control (Path) 3 Temporal Ctx	5.6	3.5	11.9	9.9	6.3
Control (Path) 4 Temporal Ctx	16.8	14.8	21.6	14.9	7.0
AD 1 Occipital Ctx	11.9	15.0	16.0	5.8	0.0

AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	8.3	8.0	10.2	7.8	0.0
AD 4 Occipital Ctx	5.8	6.8	18.6	35.4	3.5
AD 5 Occipital Ctx	25.2	12.7	22.7	16.6	3.8
AD 6 Occipital Ctx	19.8	5.9	22.1	23.5	8.5
Control 1 Occipital Ctx	6.6	4.1	7.2	15.2	1.3
Control 2 Occipital Ctx	15.7	20.3	29.3	35.8	13.7
Control 3 Occipital Ctx	5.7	7.5	19.2	4.4	5.0
Control 4 Occipital Ctx	21.6	3.3	13.6	12.9	1.3
Control (Path) 1 Occipital Ctx	28.3	25.9	39.5	22.4	12.1
Control (Path) 2 Occipital Ctx	49.7	7.4	7.0	5.0	13.2
Control (Path) 3 Occipital Ctx	0.0	2.3	5.9	6.7	9.4
Control (Path) 4 Occipital Ctx	6.6	21.0	11.4	11.9	20.4
Control 1 Parietal Ctx	8.8	12.5	15.7	33.2	5.0
Control 2 Parietal Ctx	14.5	41.2	37.1	17.4	25.5
Control 3 Parietal Ctx	19.9	13.2	10.8	21.6	16.7
Control (Path) 1 Parietal Ctx	37.6	22.5	37.9	47.3	4.2
Control (Path) 2 Parietal Ctx	16.6	26.8	18.7	17.1	14.4
Control (Path) 3 Parietal Ctx	0.0	7.5	12.0	11.7	5.9

| Control (Path) 4 Parietal Ctx | 18.2 | 20.6 | 27.9 | 29.3 | 9.4 |

Table AXH. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177
Adipose	2.6	13.2	17.3	3.7
Melanoma* Hs688(A).T	0.0	0.9	0.4	0.0
Melanoma* Hs688(B).T	0.2	1.9	2.9	0.8
Melanoma* M14	0.0	0.0	0.4	0.0
Melanoma* LOXIMVI	0.0	0.0	0.0	0.0
Melanoma* SK-MEL-5	2.2	4.4	18.3	3.0
Squamous cell carcinoma SCC-4	0.0	0.0	0.0	0.0
Testis Pool	3.5	10.0	9.1	3.0
Prostate ca.* (bone met) PC-3	0.5	1.8	1.3	1.2
Prostate Pool	1.0	10.0	28.5	2.1
Placenta	0.0	0.3	0.5	0.0
Uterus Pool	1.5	16.2	5.3	2.3
Ovarian ca. OVCAR-3	0.3	0.4	1.6	0.4
Ovarian ca. SK-OV-3	0.2	0.9	1.3	0.5
Ovarian ca. OVCAR-4	0.0	0.0	0.9	0.0
Ovarian ca. OVCAR-5	1.3	0.3	1.4	4.2
Ovarian ca. IGROV-1	100.0	27.0	69.3	100.0
Ovarian ca. OVCAR-8	21.9	7.6	17.3	18.2
Ovary	0.3	4.5	2.8	0.8
Breast ca. MCF-7	0.0	0.0	0.5	0.3
Breast ca. MDA-MB-231	0.0	0.0	0.2	0.0
Breast ca. BT 549	0.0	0.0	0.6	0.0
Breast ca. T47D	0.0	0.0	0.4	0.3

Breast ca. MDA-N	0.0	0.7	0.6	0.3
Breast Pool	4.1	42.9	12.2	3.5
Trachea	0.7	8.3	4.7	1.4
Lung	0.7	3.9	3.9	5.3
Fetal Lung	0.3	8.0	5.3	2.9
Lung ca. NCI-N417	0.9	0.2	4.0	2.0
Lung ca. LX-1	2.7	0.9	4.9	6.3
Lung ca. NCI-H146	0.0	0.0	0.1	0.0
Lung ca. SHP-77	0.4	0.2	4.5	0.8
Lung ca. A549	2.6	0.0	0.6	2.2
Lung ca. NCI-H526	0.0	0.0	0.4	0.3
Lung ca. NCI-H23	1.0	0.6	2.9	2.3
Lung ca. NCI-H460	0.0	0.0	0.0	0.0
Lung ca. HOP-62	0.0	0.0	0.5	0.0
Lung ca. NCI-H522	0.6	0.0	3.3	2.5
Liver	0.0	0.0	0.1	0.4
Fetal Liver	0.3	0.3	0.8	0.8
Liver ca. HepG2	0.3	0.0	0.1	0.9
Kidney Pool	0.0	**100.0**	43.2	14.6
Fetal Kidney	0.0	12.1	5.8	3.4
Renal ca. 786-0	0.0	0.0	0.3	0.0
Renal ca. A498	1.8	0.0	0.5	3.8
Renal ca. ACHN	0.5	0.0	1.2	0.5
Renal ca. UO-31	0.0	0.0	0.6	0.0
Renal ca. TK-10	0.4	0.7	2.1	0.5
Bladder	0.0	6.6	8.3	0.9
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.1	0.8
Gastric ca. KATO III	0.5	0.3	0.4	0.4
Colon ca. SW-948	1.5	0.0	0.3	2.2
Colon ca. SW480	5.2	4.4	23.0	6.3

Colon ca.* (SW480 met) SW620	4.8	1.7	6.1	7.2
Colon ca. HT29	0.0	0.0	0.0	0.3
Colon ca. HCT-116	0.2	0.5	2.1	0.6
Colon ca. CaCo-2	3.6	7.6	18.3	6.5
Colon cancer tissue	3.3	5.6	7.7	4.4
Colon ca. SW1116	3.0	1.1	1.8	2.1
Colon ca. Colo-205	0.4	0.0	0.2	1.3
Colon ca. SW-48	3.6	0.0	1.4	3.0
Colon Pool	5.0	44.8	25.5	8.1
Small Intestine Pool	1.7	26.8	12.8	2.0
Stomach Pool	2.3	24.0	8.5	4.2
Bone Marrow Pool	1.6	25.9	18.7	3.5
Fetal Heart	2.3	31.6	33.7	8.6
Heart Pool	7.0	23.5	33.7	10.7
Lymph Node Pool	6.1	64.6	19.9	6.7
Fetal Skeletal Muscle	5.2	46.7	19.1	19.2
Skeletal Muscle Pool	9.2	24.7	22.1	22.7
Spleen Pool	0.0	2.4	2.7	0.6
Thymus Pool	2.0	18.4	7.7	3.1
CNS cancer (glio/astro) U87-MG	1.5	5.8	10.9	2.2
CNS cancer (glio/astro) U-118-MG	0.3	1.5	3.8	0.8
CNS cancer (neuro;met) SK-N-AS	0.0	0.7	1.4	0.5
CNS cancer (astro) SF-539	0.0	0.2	0.1	0.2
CNS cancer (astro) SNB-75	1.1	3.1	11.7	2.8
CNS cancer (glio) SNB-19	79.0	12.8	100.0	97.9
CNS cancer (glio) SF-295	0.0	0.0	8.2	1.5

Brain (Amygdala) Pool	0.8	7.9	8.0	4.4
Brain (cerebellum)	0.4	1.8	8.8	1.2
Brain (fetal)	0.7	8.4	6.8	2.1
Brain (Hippocampus) Pool	3.2	9.9	11.0	4.3
Cerebral Cortex Pool	0.6	1.8	11.6	2.0
Brain (Substantia nigra) Pool	2.2	4.2	10.0	2.0
Brain (Thalamus) Pool	2.7	9.1	9.7	2.8
Brain (whole)	0.4	3.3	5.6	1.9
Spinal Cord Pool	2.3	13.1	12.2	4.2
Adrenal Gland	0.3	7.4	4.8	0.9
Pituitary gland Pool	0.0	1.8	1.4	0.6
Salivary Gland	0.0	2.3	1.1	0.0
Thyroid (female)	0.3	3.3	1.9	1.3
Pancreatic ca. CAPAN2	0.0	0.5	0.7	0.6
Pancreas Pool	0.0	3.5	3.2	1.0

Table AXI. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6439, Run 268760823	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.0	0.0	0.0	0.0
Secondary Th2 act	0.0	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.7	0.0	0.0
Secondary Tr1 rest	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0
Primary Th2 act	0.0	0.7	0.0	0.0
Primary Tr1 act	0.0	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	1.2	0.0
Primary Th2 rest	0.0	0.0	0.0	0.0

Primary Tr1 rest	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	0.8	2.6	0.0
CD45RO CD4 lymphocyte act	0.0	1.6	2.3	0.0
CD8 lymphocyte act	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	0.0	0.0
CD4 lymphocyte none	0.0	0.0	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	1.2	0.0
LAK cells rest	2.7	6.1	15.2	0.0
LAK cells IL-2	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	6.1	9.0	0.0
NK Cells IL-2 rest	0.0	0.0	1.4	0.0
Two Way MLR 3 day	0.0	0.9	1.4	0.0
Two Way MLR 5 day	0.0	0.0	0.0	0.0
Two Way MLR 7 day	13.2	2.9	3.7	0.0
PBMC rest	0.0	0.0	0.0	0.0
PBMC PWM	0.0	0.0	0.0	0.0
PBMC PHA-L	0.0	0.0	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	9.1	0.0	68.8	0.0

EOL-1 dbcAMP PMA/ionomycin	0.0	1.0	1.8	0.0
Dendritic cells none	13.8	0.7	0.0	0.0
Dendritic cells LPS	0.0	0.0	0.0	0.0
Dendritic cells anti-CD40	3.3	1.6	0.0	0.0
Monocytes rest	0.0	0.0	0.0	0.0
Monocytes LPS	0.0	0.0	2.6	0.4
Macrophages rest	0.0	0.0	0.0	0.0
Macrophages LPS	0.0	0.8	9.2	0.0
HUVEC none	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.6	0.0	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0	0.0
Lung Microvascular EC none	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.5	0.0	0.3
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.0	0.0	0.0
Astrocytes rest	100.0	100.0	100.0	54.3

Astrocytes TNFalpha + IL-1beta	74.2	97.9	95.9	100.0
KU-812 (Basophil) rest	0.0	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0	0.0
Liver cirrhosis	4.6	5.1	8.5	0.6
NCI-H292 none	0.0	0.0	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0	0.0
NCI-H292 IL-9	0.0	0.0	0.0	0.0
NCI-H292 IL-13	0.0	0.0	0.0	0.0
NCI-H292 IFN gamma	0.0	0.0	0.0	0.0
HPAEC none	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0	0.0
Lung fibroblast none	31.4	62.9	94.0	26.2
Lung fibroblast TNF alpha + IL-1 beta	22.2	25.2	62.9	28.3
Lung fibroblast IL-4	19.1	23.3	34.9	16.0
Lung fibroblast IL-9	23.5	20.4	96.6	9.3
Lung fibroblast IL-13	4.5	15.0	13.4	4.3
Lung fibroblast IFN gamma	15.7	29.9	89.5	25.2
Dermal fibroblast CCD1070 rest	0.0	5.6	4.1	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	0.8	2.3	1.1
Dermal fibroblast CCD1070 IL-1 beta	0.0	0.7	0.0	1.6
Dermal fibroblast IFN gamma	8.5	20.0	26.6	4.9
Dermal fibroblast IL-4	4.1	22.7	25.5	13.5
Dermal Fibroblasts rest	8.0	20.7	47.3	15.8

Neutrophils TNFa+LPS	0.0	1.2	0.0	0.0
Neutrophils rest	0.0	0.0	0.0	0.0
Colon	4.0	7.9	8.4	4.8
Lung	0.0	1.6	2.1	0.0
Thymus	0.0	2.0	2.4	0.0
Kidney	4.9	10.2	5.2	0.6

CNS_neurodegeneration_v1.0 Summary: Ag6425/Ag6435/Ag6439/Ag6440/ Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6426 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

General_screening_panel_v1.6 Summary: Ag6425/Ag6435/Ag6439/Ag6440 Four experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in kidney, a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-30). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6447 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag6425/Ag6435/Ag6439/Ag6447 Four experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=31-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types

5   and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Ag6426/ Ag6440 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

10   **AY. CG56054-18: Integrin alpha 7-like protein.**

Expression of gene CG56054-18 was assessed using the primer-probe sets Ag4983, Ag6442, Ag6425, Ag6428, Ag6431, Ag6435, Ag6439, Ag6447, Ag6413 and Ag6964, described in Tables AYA, AYB, AYC, AYD, AYE, AYF, AYG, AYH, AYI and AYJ. Results of the RTQ-PCR runs are shown in Tables AYK, AYL, AYM, AYN, AYO and

15   AYP.

Table AYA. Probe Name Ag4983

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccaggtcaccttctacctcatc-3'	22	2342	708
Probe	TET-5'-cttagcacctccgggatcagcatt-3'-TAMRA	24	2364	709
Reverse	5'-aacagcagctctacctccagtt-3'	22	2398	710

Table AYB. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	2781	711
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	2820	712
Reverse	5'-gcgcagtccagggtg-3'	15	2906	713

Table AYC. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacaccccat-3'	16	3296	714
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	3328	715
Reverse	5'-gccctggatgcccat-3'	15	3347	716

Table AYD. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1301	717
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1341	718
Reverse	5'-agggagtagccgaagctct-3'	19	1378	719

Table AYE. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2900	720
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2941	721
Reverse	5'-ccgcgcggtcaaa-3'	13	2967	722

Table AYF. Probe Name Ag6435

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccagggtggagct-3'	15	731	723
Probe	TET-5'-acctggcacacctggacgacg-3'-TAMRA	21	766	724
Reverse	5'-cagggaccgggatga-3'	15	829	725

5

Table AYG. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No

Forward	5'-ctgtggtggcagaaggagt-3'	19	3157	726
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	3177	727
Reverse	5'-gaagaatcccatcttccacag-3'	21	3243	728

Table AYH. Probe Name Ag6447

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gacgacggtccctacga-3'	17	780	729
Probe	TET-5'-tcatcccggtccctgccaa-3'-TAMRA	19	829	730
Reverse	5'-gtcaatagagaagccaaagtagct-3'	24	849	731

Table AYI. Probe Name Ag6413

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggtgaagacaagatctgccag-3'	21	1980	732
Probe	TET-5'-tgtacccgggtcagcgacacg-3'-TAMRA	21	2031	733
Reverse	5'-gctgttgttccatccacatc-3'	20	2073	734

Table AYJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2986	735
Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2957	736
Reverse	5'-gccaactgtgtggtgttca-3'	19	2931	737

5   Table AYK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag4983, Run 218649223	Rel. Exp.(%) Ag6413, Run 269253983	Rel. Exp.(%) Ag6425, Run 266937076	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6435, Run 269253997	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6442, Run 264979298	Rel. Exp.(%) Ag6447, Run 269254007
AD 1 Hippo	23.7	24.8	24.1	18.0	18.8	17.1	21.6	19.2	18.8
AD 2 Hippo	41.2	52.9	48.0	32.3	28.7	27.9	28.9	49.7	10.4
AD 3 Hippo	8.9	6.4	6.5	3.7	7.5	4.8	6.1	20.4	0.0
AD 4 Hippo	14.8	25.5	13.8	10.7	18.8	18.3	17.6	5.6	4.6
AD 5 Hippo	44.8	41.8	52.9	53.2	38.4	46.7	42.6	57.4	11.0
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.1	100.0
Control 2 Hippo	24.3	36.1	10.6	18.7	29.5	8.5	32.5	28.5	3.1
Control 4 Hippo	42.9	43.8	51.8	27.0	32.3	29.9	37.9	86.5	43.8
Control (Path) 3 Hippo	14.2	11.4	9.8	4.6	6.0	5.2	6.4	0.0	5.3
AD 1 Temporal Ctx	23.3	15.9	10.1	12.9	17.1	12.8	24.5	16.8	9.0
AD 2 Temporal Ctx	41.5	47.3	33.7	31.0	39.8	45.1	27.5	21.6	21.0
AD 3 Temporal Ctx	9.5	9.8	0.0	6.0	11.3	4.1	9.0	5.7	3.9
AD 4 Temporal Ctx	30.6	39.0	12.8	20.2	25.3	6.8	30.4	8.7	7.7
AD 5 Inf Temporal Ctx	45.4	37.1	59.0	39.2	36.3	1.6	41.8	73.7	23.7

AD 5 Sup Temporal Ctx	51.1	39.0	21.9	42.0	32.3	33.2	38.7	55.9	11.4
AD 6 Inf Temporal Ctx	38.2	59.9	73.7	49.3	46.7	52.1	47.6	76.8	88.9
AD 6 Sup Temporal Ctx	43.8	48.6	50.3	48.3	50.3	37.6	50.3	59.9	61.1
Control 1 Temporal Ctx	12.2	23.0	11.9	12.9	15.6	6.7	24.0	46.7	2.8
Control 2 Temporal Ctx	14.2	32.5	18.6	18.2	17.4	7.3	14.9	50.0	16.0
Control 3 Temporal Ctx	15.1	15.3	6.0	9.6	14.5	4.4	16.5	9.5	3.1
Control 3 Temporal Ctx	23.7	25.0	25.7	15.2	13.1	11.7	23.8	13.6	13.6
Control (Path) 1 Temporal Ctx	26.1	47.0	18.0	27.0	30.6	24.8	39.8	46.0	13.8
Control (Path) 2 Temporal Ctx	24.5	25.9	18.4	16.0	20.4	9.8	24.8	0.0	2.6
Control (Path) 3 Temporal Ctx	11.7	16.0	5.6	7.5	10.9	3.5	11.9	31.0	6.3
Control (Path) 4 Temporal Ctx	21.9	27.4	16.8	17.1	18.2	14.8	21.6	39.5	7.0
AD 1 Occipital Ctx	16.0	11.9	11.9	10.2	11.5	15.0	16.0	6.3	0.0
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

AD 3 Occipital Ctx	10.7	6.0	8.3	6.4	8.8	8.0	10.2	4.9	0.0
AD 4 Occipital Ctx	18.9	23.7	5.8	13.0	17.9	6.8	18.6	11.1	3.5
AD 5 Occipital Ctx	24.8	28.3	25.2	25.3	22.5	12.7	22.7	42.3	3.8
AD 6 Occipital Ctx	20.6	31.9	19.8	20.2	17.0	5.9	22.1	14.8	8.5
Control 1 Occipital Ctx	9.5	14.4	6.6	6.0	8.7	4.1	7.2	8.8	1.3
Control 2 Occipital Ctx	31.9	42.6	15.7	26.4	33.2	20.3	29.3	82.4	13.7
Control 3 Occipital Ctx	18.8	13.0	5.7	10.7	17.1	7.5	19.2	8.8	5.0
Control 4 Occipital Ctx	18.2	17.0	21.6	12.0	12.6	3.3	13.6	24.0	1.3
Control (Path) 1 Occipital Ctx	38.2	52.5	28.3	35.6	36.1	25.9	39.5	100.0	12.1
Control (Path) 2 Occipital Ctx	9.6	14.1	49.7	6.7	7.9	7.4	7.0	9.3	13.2
Control (Path) 3 Occipital Ctx	4.8	8.7	0.0	5.4	6.0	2.3	5.9	4.1	9.4
Control (Path) 4 Occipital Ctx	16.2	13.2	6.6	13.2	10.2	21.0	11.4	32.8	20.4
Control 1 Parietal Ctx	14.4	21.9	8.8	8.8	16.3	12.5	15.7	9.2	5.0

Control 2 Parietal Ctx	32.8	28.9	14.5	34.4	28.3	41.2	37.1	28.1	25.5
Control 3 Parietal Ctx	20.6	19.8	19.9	11.5	8.7	13.2	10.8	9.1	16.7
Control (Path) 1 Parietal Ctx	35.4	62.4	37.6	34.2	39.2	22.5	37.9	69.3	4.2
Control (Path) 2 Parietal Ctx	22.1	23.8	16.6	19.6	22.5	26.8	18.7	37.6	14.4
Control (Path) 3 Parietal Ctx	11.2	15.4	0.0	3.9	7.1	7.5	12.0	10.4	5.9
Control (Path) 4 Parietal Ctx	31.2	34.2	18.2	24.8	8.8	20.6	27.9	27.5	9.4

Table AYL. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386	Tissue Name	Rel. Exp.(%) Ag4983, Run 218328386
Adipose	25.3	Renal ca. TK-10	3.0
Melanoma* Hs688(A).T	1.0	Bladder	7.0
Melanoma* Hs688(B).T	2.9	Gastric ca. (liver met.) NCI-N87	1.9
Melanoma* M14	0.7	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	29.9	Colon ca. SW480	45.4
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	17.1
Testis Pool	10.7	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	2.9	Colon ca. HCT-116	5.3
Prostate Pool	18.4	Colon ca. CaCo-2	21.8

Placenta	0.4	Colon cancer tissue	12.7
Uterus Pool	10.4	Colon ca. SW1116	2.4
Ovarian ca. OVCAR-3	1.2	Colon ca. Colo-205	0.4
Ovarian ca. SK-OV-3	1.7	Colon ca. SW-48	1.5
Ovarian ca. OVCAR-4	0.6	Colon Pool	31.4
Ovarian ca. OVCAR-5	2.1	Small Intestine Pool	12.1
Ovarian ca. IGROV-1	87.7	Stomach Pool	13.6
Ovarian ca. OVCAR-8	10.6	Bone Marrow Pool	13.2
Ovary	4.7	Fetal Heart	24.1
Breast ca. MCF-7	0.4	Heart Pool	34.9
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	26.4
Breast ca. BT 549	0.6	Fetal Skeletal Muscle	55.1
Breast ca. T47D	5.1	Skeletal Muscle Pool	82.4
Breast ca. MDA-N	1.0	Spleen Pool	3.3
Breast Pool	18.2	Thymus Pool	10.2
Trachea	8.9	CNS cancer (glio/astro) U87-MG	14.9
Lung	3.7	CNS cancer (glio/astro) U-118-MG	5.1
Fetal Lung	7.2	CNS cancer (neuro;met) SK-N-AS	2.6
Lung ca. NCI-N417	2.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	9.7	CNS cancer (astro) SNB-75	11.9
Lung ca. NCI-H146	0.3	CNS cancer (glio) SNB-19	100.0
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-295	14.6
Lung ca. A549	0.7	Brain (Amygdala) Pool	8.0
Lung ca. NCI-H526	0.4	Brain (cerebellum)	11.5
Lung ca. NCI-H23	6.4	Brain (fetal)	10.8
Lung ca. NCI-H460	0.2	Brain (Hippocampus) Pool	11.6
Lung ca. HOP-62	0.9	Cerebral Cortex Pool	12.9

Lung ca. NCI-H522	2.2	Brain (Substantia nigra) Pool	15.9
Liver	0.2	Brain (Thalamus) Pool	13.7
Fetal Liver	0.6	Brain (whole)	7.7
Liver ca. HepG2	0.3	Spinal Cord Pool	14.9
Kidney Pool	41.8	Adrenal Gland	7.9
Fetal Kidney	4.9	Pituitary gland Pool	1.3
Renal ca. 786-0	0.3	Salivary Gland	1.6
Renal ca. A498	0.4	Thyroid (female)	3.0
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	1.5
Renal ca. UO-31	0.6	Pancreas Pool	16.0

Table AYM. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3

Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	**100.0**
Breast ca. MDA-N	0.5	Spleen Pool	1.9
Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0

Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AYN. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6413, Run 277249371	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6435, Run 277223167	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	25.9	2.6	20.0	17.4	13.8	13.2	17.3	18.8
Melanoma* Hs688(A).T	0.5	0.0	2.0	0.8	0.9	0.9	0.4	0.7
Melanoma* Hs688(B).T	2.7	0.2	4.1	2.5	2.2	1.9	2.9	2.4
Melanoma* M14	0.3	0.0	0.7	0.4	0.4	0.0	0.4	0.7
Melanoma* LOXIMVI	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	15.2	2.2	30.4	18.2	14.6	4.4	18.3	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.1	0.2	0.0	0.0	0.1
Testis Pool	5.2	3.5	8.8	10.4	9.0	10.0	9.1	9.9
Prostate ca.* (bone met) PC-3	1.9	0.5	2.5	1.9	1.8	1.8	1.3	4.3
Prostate Pool	8.1	1.0	11.5	11.3	12.1	10.0	28.5	10.0
Placenta	0.5	0.0	0.7	0.1	0.1	0.3	0.5	0.4
Uterus Pool	2.2	1.5	4.5	4.6	4.5	16.2	5.3	4.1
Ovarian ca. OVCAR-3	0.9	0.3	1.1	0.7	1.1	0.4	1.6	4.0

Ovarian ca. SK-OV-3	0.8	0.2	1.7	0.8	0.9	0.9	1.3	1.7
Ovarian ca. OVCAR-4	0.2	0.0	0.9	0.4	0.8	0.0	0.9	0.5
Ovarian ca. OVCAR-5	1.6	1.3	2.9	1.3	1.7	0.3	1.4	7.9
Ovarian ca. IGROV-1	**100.0**	**100.0**	77.9	84.7	97.9	27.0	69.3	75.8
Ovarian ca. OVCAR-8	13.6	21.9	14.0	15.6	14.6	7.6	17.3	16.7
Ovary	2.7	0.3	5.2	3.1	2.3	4.5	2.8	2.4
Breast ca. MCF-7	0.3	0.0	0.3	0.1	0.2	0.0	0.5	0.5
Breast ca. MDA-MB-231	0.1	0.0	0.4	0.2	0.2	0.0	0.2	0.3
Breast ca. BT 549	0.5	0.0	0.5	0.1	0.5	0.0	0.6	0.4
Breast ca. T47D	0.0	0.0	0.5	0.2	0.3	0.0	0.4	0.5
Breast ca. MDA-N	0.6	0.0	0.7	0.6	0.6	0.7	0.6	0.8
Breast Pool	15.0	4.1	21.8	14.6	10.7	42.9	12.2	16.7
Trachea	4.5	0.7	8.4	4.8	4.2	8.3	4.7	5.6
Lung	2.8	0.7	2.3	4.2	3.2	3.9	3.9	5.1
Fetal Lung	3.9	0.3	9.1	5.0	4.8	8.0	5.3	6.1
Lung ca. NCI-N417	2.0	0.9	3.5	3.3	2.6	0.2	4.0	2.3
Lung ca. LX-1	3.5	2.7	6.5	5.0	3.5	0.9	4.9	44.1
Lung ca. NCI-H146	0.1	0.0	0.3	0.1	0.2	0.0	0.1	0.1
Lung ca. SHP-77	4.0	0.4	6.8	5.3	4.5	0.2	4.5	3.8
Lung ca. A549	0.3	2.6	0.9	0.0	0.4	0.0	0.6	4.7
Lung ca. NCI-H526	0.2	0.0	0.9	0.6	0.3	0.0	0.4	0.5

Lung ca. NCI-H23	2.9	1.0	4.6	4.8	3.2	0.6	2.9	10.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.1	0.3	0.0	0.0	0.3
Lung ca. HOP-62	0.5	0.0	0.5	1.0	0.6	0.0	0.5	0.7
Lung ca. NCI-H522	1.7	0.6	2.3	1.7	1.3	0.0	3.3	8.9
Liver	0.1	0.0	0.0	0.0	0.0	0.0	0.1	2.0
Fetal Liver	0.3	0.3	1.1	0.6	0.5	0.3	0.8	8.2
Liver ca. HepG2	0.1	0.3	0.2	0.0	0.2	0.0	0.1	2.4
Kidney Pool	27.9	0.0	47.0	33.9	28.1	100.0	43.2	32.8
Fetal Kidney	1.4	0.0	4.9	4.1	4.0	12.1	5.8	11.5
Renal ca. 786-0	0.2	0.0	0.2	0.3	0.1	0.0	0.3	0.9
Renal ca. A498	0.0	1.8	0.2	0.0	0.3	0.0	0.5	8.5
Renal ca. ACHN	1.5	0.5	2.5	1.7	1.5	0.0	1.2	2.5
Renal ca. UO-31	0.3	0.0	0.5	0.2	0.2	0.0	0.6	0.3
Renal ca. TK-10	1.9	0.4	3.1	2.0	1.9	0.7	2.1	4.6
Bladder	4.2	0.0	5.9	5.5	5.1	6.6	8.3	6.7
Gastric ca. (liver met.) NCI-N87	0.9	0.0	1.7	0.9	1.2	0.0	1.1	6.7
Gastric ca. KATO III	0.4	0.5	0.8	0.2	0.3	0.3	0.4	0.9
Colon ca. SW-948	0.0	1.5	0.2	0.2	0.2	0.0	0.3	1.2
Colon ca. SW480	20.9	5.2	41.8	27.0	23.3	4.4	23.0	33.7
Colon ca.* (SW480 met) SW620	13.3	4.8	16.4	12.8	10.3	1.7	6.1	25.0
Colon ca. HT29	0.2	0.0	0.0	0.2	0.2	0.0	0.0	0.3

Colon ca. HCT-116	2.1	0.2	3.2	2.5	2.0	0.5	2.1	4.3
Colon ca. CaCo-2	15.0	3.6	27.0	19.1	16.7	7.6	18.3	38.2
Colon cancer tissue	9.0	3.3	11.0	11.9	7.6	5.6	7.7	20.4
Colon ca. SW1116	1.3	3.0	2.5	2.0	1.5	1.1	1.8	6.0
Colon ca. Colo-205	0.1	0.4	0.3	0.2	0.0	0.0	0.2	0.8
Colon ca. SW-48	0.8	3.6	1.4	1.5	1.5	0.0	1.4	2.6
Colon Pool	20.3	5.0	28.1	23.2	18.7	44.8	25.5	20.6
Small Intestine Pool	14.0	1.7	17.1	11.2	13.0	26.8	12.8	10.4
Stomach Pool	8.1	2.3	14.3	9.5	9.3	24.0	8.5	10.7
Bone Marrow Pool	6.8	1.6	14.3	10.2	8.7	25.9	18.7	12.5
Fetal Heart	10.1	2.3	25.5	24.5	21.8	31.6	33.7	20.7
Heart Pool	28.7	7.0	29.7	25.9	17.2	23.5	33.7	26.1
Lymph Node Pool	17.6	6.1	33.7	22.1	23.7	64.6	19.9	24.7
Fetal Skeletal Muscle	31.9	5.2	54.3	48.6	46.3	46.7	19.1	50.7
Skeletal Muscle Pool	17.4	9.2	29.3	29.5	25.9	24.7	22.1	32.3
Spleen Pool	0.9	0.0	1.9	2.0	1.7	2.4	2.7	3.1
Thymus Pool	4.4	2.0	10.4	8.1	9.4	18.4	7.7	7.0
CNS cancer (glio/astro) U87-MG	9.8	1.5	14.9	10.7	10.0	5.8	10.9	14.1
CNS cancer (glio/astro) U-118-MG	3.5	0.3	4.7	3.8	3.1	1.5	3.8	5.8
CNS cancer (neuro;met) SK-N-AS	1.9	0.0	2.6	2.1	1.0	0.7	1.4	2.6
CNS cancer (astro) SF-539	0.1	0.0	0.0	0.1	0.2	0.2	0.1	0.1

CNS cancer (astro) SNB-75	8.1	1.1	14.9	6.5	10.0	3.1	11.7	9.7
CNS cancer (glio) SNB-19	79.6	79.0	100.0	100.0	100.0	12.8	100.0	100.0
CNS cancer (glio) SF-295	8.2	0.0	11.3	8.0	7.8	0.0	8.2	14.8
Brain (Amygdala) Pool	3.7	0.8	7.7	6.2	4.8	7.9	8.0	5.3
Brain (cerebellum)	12.0	0.4	19.8	10.7	9.7	1.8	8.8	9.7
Brain (fetal)	4.2	0.7	12.7	6.6	5.6	8.4	6.8	6.4
Brain (Hippocampus) Pool	7.5	3.2	11.7	8.6	6.9	9.9	11.0	10.2
Cerebral Cortex Pool	9.7	0.6	11.0	7.5	0.7	1.8	11.6	8.7
Brain (Substantia nigra) Pool	7.4	2.2	11.7	10.4	4.7	4.2	10.0	9.3
Brain (Thalamus) Pool	7.6	2.7	13.2	9.3	0.2	9.1	9.7	8.7
Brain (whole)	6.1	0.4	10.6	5.8	0.3	3.3	5.6	8.7
Spinal Cord Pool	10.1	2.3	14.7	11.0	7.6	13.1	12.2	9.0
Adrenal Gland	3.5	0.3	9.9	3.9	3.7	7.4	4.8	4.1
Pituitary gland Pool	0.9	0.0	1.1	1.2	1.1	1.8	1.4	0.5
Salivary Gland	0.9	0.0	1.8	1.3	0.9	2.3	1.1	1.0
Thyroid (female)	2.0	0.3	3.1	2.5	2.5	3.3	1.9	2.3
Pancreatic ca. CAPAN2	0.5	0.0	0.8	0.7	0.6	0.5	0.7	2.2
Pancreas Pool	1.2	0.0	2.0	1.1	1.6	3.5	3.2	2.3

Table AYO. Panel 4.1D

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Tissue Name	Rel. Exp.(%) Ag4983, Run 218623570	Rel. Exp.(%) Ag6413, Run 269239947	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6435, Run 268713480	Rel. Exp.(%) Ag6439, Run 268760823	Rel. Exp.(%) Ag6447, Run 268761806
Secondary Th1 act	0.1	0.3	0.0	1.3	0.7	0.0	0.0	0.0
Secondary Th2 act	0.5	0.3	0.0	1.2	0.8	0.0	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.0	0.7	0.0	0.0	0.0
Secondary Th1 rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.3	0.0	0.0	0.0	0.0	0.7	0.0	0.0
Secondary Tr1 rest	0.1	0.3	0.0	0.4	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.2	0.4	0.0	0.3	0.4	0.7	0.0	0.0
Primary Tr1 act	0.1	0.0	0.0	0.7	0.7	0.0	0.0	0.0
Primary Th1 rest	0.0	0.0	0.0	0.1	0.3	0.0	1.2	0.0
Primary Th2 rest	0.0	0.0	0.0	0.4	0.2	0.0	0.0	0.0
Primary Tr1 rest	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.4	2.8	0.0	5.4	2.4	0.8	2.6	0.0
CD45RO CD4 lymphocyte act	0.1	2.2	0.0	1.5	0.7	1.6	2.3	0.0
CD8 lymphocyte act	0.4	0.9	0.0	0.7	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.1	0.0	0.0	8.8	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.1	0.0	0.4	0.3	0.0 .	0.0	0.0
CD4 lymphocyte none	0.1	0.0	0.0	0.5	0.4	0.0	0.0	0.0

2ry Th1/Th2/Tr1_a nti-CD95 CH11	0.3	0.2	0.0	0.0	0.0	0.0	1.2	0.0
LAK cells rest	5.6	5.0	2.7	11.8	3.8	6.1	15.2	0.0
LAK cells IL-2	0.4	0.3	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IFN gamma	0.1	0.3	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomyci n	4.5	4.0	15.7	15.1	6.3	6.1	9.0	0.0
NK Cells IL-2 rest	0.9	0.1	0.0	3.4	2.5	0.0	1.4	0.0
Two Way MLR 3 day	1.4	1.1	0.0	2.2	1.3	0.9	1.4	0.0
Two Way MLR 5 day	4.5	0.9	0.0	0.8	0.9	0.0	0.0	0.0
Two Way MLR 7 day	2.3	0.7	13.2	1.1	2.6	2.9	3.7	0.0
PBMC rest	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.6	0.0	0.0	1.3	0.0	0.0	0.0	0.0
PBMC PHA-L	0.3	0.2	0.0	0.6	0.7	0.0	0.0	0.0
Ramos (B cell) none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	0.0	0.7	0.2	0.0	0.0	0.0
B lymphocytes PWM	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.2	0.0	0.0	0.9	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	3.7	2.6	9.1	29.1	8.1	0.0	68.8	0.0

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EOL-1 dbcAMP PMA/ionomycin	1.6	0.7	0.0	0.0	2.7	1.0	1.8	0.0
Dendritic cells none	5.6	3.1	13.8	4.1	5.3	0.7	0.0	0.0
Dendritic cells LPS	1.6	0.3	0.0	1.0	0.7	0.0	0.0	0.0
Dendritic cells anti-CD40	2.0	1.6	3.3	0.5	0.2	1.6	0.0	0.0
Monocytes rest	0.2	0.0	0.0	0.4	0.0	0.0	0.0	0.0
Monocytes LPS	2.2	3.3	0.0	5.7	1.8	0.0	2.6	0.4
Macrophages rest	0.9	1.8	0.0	0.6	0.6	0.0	0.0	0.0
Macrophages LPS	7.5	4.0	0.0	5.4	6.3	0.8	9.2	0.0
HUVEC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0
HUVEC IL-1beta	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0
HUVEC IFN gamma	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.6	0.0	0.0
HUVEC TNF alpha + IL4	0.6	0.0	0.0	0.0	0.4	0.0	0.0	0.0
HUVEC IL-11	0.0	0.0	0.0	0.4	0.3	0.0	0.0	0.0
Lung Microvascular EC none	0.2	0.3	0.0	0.4	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Microsvasular Dermal EC TNFalpha + IL-1 beta	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1 beta	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1 beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.1	0.6	0.0	0.0	0.0	0.5	0.0	0.3
Coronery artery SMC TNFalpha + IL-1 beta	0.4	0.9	6.2	0.3	1.5	0.0	0.0	0.0
Astrocytes rest	67.8	97.3	100.0	100.0	100.0	100.0	100.0	54.3
Astrocytes TNFalpha + IL-1 beta	100.0	100.0	74.2	97.3	74.7	97.9	95.9	100.0
KU-812 (Basophil) rest	0.1	0.0	0.0	0.0	0.4	0.0	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
CCD1106 (Keratinocytes) none	0.2	0.0	0.0	0.0	0.8	0.0	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1 beta	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	2.3	7.2	4.6	2.6	6.7	5.1	8.5	0.6
NCI-H292 none	0.3	0.3	0.0	1.7	0.6	0.0	0.0	0.0
NCI-H292 IL-4	0.3	0.0	0.0	0.0	0.5	0.0	0.0	0.0
NCI-H292 IL-9	0.3	0.0	0.0	0.7	0.5	0.0	0.0	0.0

NCI-H292 IL-13	0.6	0.6	0.0	0.9	0.9	0.0	0.0	0.0
NCI-H292 IFN gamma	0.2	0.0	0.0	0.5	0.6	0.0	0.0	0.0
HPAEC none	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
Lung fibroblast none	29.7	62.9	31.4	95.9	65.5	62.9	94.0	26.2
Lung fibroblast TNF alpha + IL-1 beta	16.0	36.9	22.2	48.6	39.8	25.2	62.9	28.3
Lung fibroblast IL-4	26.1	28.7	19.1	27.4	21.2	23.3	34.9	16.0
Lung fibroblast IL-9	28.5	42.0	23.5	24.0	26.8	20.4	96.6	9.3
Lung fibroblast IL-13	31.6	14.6	4.5	11.9	10.4	15.0	13.4	4.3
Lung fibroblast IFN gamma	20.4	32.8	15.7	55.9	46.3	29.9	89.5	25.2
Dermal fibroblast CCD1070 rest	2.5	2.9	0.0	6.0	6.3	5.6	4.1	0.0
Dermal fibroblast CCD1070 TNF alpha	1.1	1.3	0.0	2.7	0.8	0.8	2.3	1.1
Dermal fibroblast CCD1070 IL-1 beta	1.9	2.9	0.0	5.6	1.3	0.7	0.0	1.6
Dermal fibroblast IFN gamma	9.3	20.3	8.5	30.6	20.2	20.0	26.6	4.9
Dermal fibroblast IL-4	10.7	14.6	4.1	30.8	19.8	22.7	25.5	13.5
Dermal Fibroblasts rest	24.8	42.3	8.0	54.3	46.7	20.7	47.3	15.8
Neutrophils TNFa+LPS	0.7	0.0	0.0	0.9	0.4	1.2	0.0	0.0

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Neutrophils rest	0.1	0.0	0.0	0.0	0.3	0.0	0.0	0.0
Colon	7.9	4.7	4.0	4.6	9.5	7.9	8.4	4.8
Lung	2.2	1.2	0.0	2.8	4.6	1.6	2.1	0.0
Thymus	3.1	0.8	0.0	0.0	0.4	2.0	2.4	0.0
Kidney	4.2	4.4	4.9	7.8	9.7	10.2	5.2	0.6

Table AYP. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag4983, Run 260281959	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	12.1	22.7	Bladder NAT 2	1.7	1.4
Colon NAT 1	100.0	100.0	Bladder NAT 3	0.2	4.8
Colon cancer 2	6.5	0.0	Bladder NAT 4	27.0	66.0
Colon NAT 2	8.0	15.1	Prostate adenocarcinoma 1	9.2	7.5
Colon cancer 3	7.4	2.8	Prostate adenocarcinoma 2	3.5	8.0
Colon NAT 3	39.8	40.1	Prostate adenocarcinoma 3	14.3	9.0
Colon malignant cancer 4	15.0	9.5	Prostate adenocarcinoma 4	16.4	9.1
Colon NAT 4	3.5	0.9	Prostate NAT 5	16.8	9.9
Lung cancer 1	1.4	6.6	Prostate adenocarcinoma 6	3.2	7.7
Lung NAT 1	0.6	0.0	Prostate adenocarcinoma 7	9.2	17.3
Lung cancer 2	26.6	15.9	Prostate adenocarcinoma 8	3.0	0.0
Lung NAT 2	2.7	0.0	Prostate adenocarcinoma 9	27.0	33.9
Squamous cell carcinoma 3	5.6	8.3	Prostate NAT 10	3.8	4.9
Lung NAT 3	0.8	0.0	Kidney cancer 1	24.0	16.5
Metastatic melanoma 1	27.2	49.0	Kidney NAT 1	15.6	7.2
Melanoma 2	2.5	1.1	Kidney cancer 2	91.4	73.7
Melanoma 3	2.3	13.8	Kidney NAT 2	22.1	19.2

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Metastatic melanoma 4	33.9	24.0	Kidney cancer 3	27.0	21.3
Metastatic melanoma 5	34.6	31.4	Kidney NAT 3	9.3	11.4
Bladder cancer 1	1.3	2.1	Kidney cancer 4	20.0	25.7
Bladder NAT 1	0.0	0.0	Kidney NAT 4	8.2	14.9
Bladder cancer 2	8.7	19.3			

CNS_neurodegeneration_v1.0 Summary: Ag4983/Ag6413/ Ag6425/Ag6428/Ag6431/ Ag6435/Ag6439/Ag6442/ Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals.

5 However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag4983 Highest expression of this gene is detected in a brain cancer SNB-19 cell line (CT=28). Moderate to low levels of

10 expression of this gene is also seen in a number of cancer cell lines derived from gastric, colon, lung, renal, breast, ovarian, prostate, melanoma and brain cancers. Thus, expression of this gene could be used as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of pancreatic, gastric, colon, lung, liver, renal, breast, ovarian, prostate, squamous

15 cell carcinoma, melanoma and brain cancers.

Among tissues with metabolic or endocrine function, this gene is expressed at moderate levels in pancreas, adipose, adrenal gland, thyroid, pituitary gland, skeletal muscle, heart and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases,

20 such as obesity and diabetes.

In addition, this gene is expressed at moderate levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, therapeutic modulation of this gene product may be useful in the treatment of central nervous system disorders such as

Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28)

5   as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers.

10   This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

General_screening_panel_v1.6
Summary: Ag6413/Ag6425/Ag6428/Ag6431/Ag6435/Ag6439/Ag6964 Eight experiments with seven different probe and primer sets are in very good agreement. Highest expression

15   of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

20   Ag6442 Expression of this gene is low/undetectable (CTs > 34.9) across all of the samples on this panel (data not shown).

Panel 4.1D
Summary: Ag4983/Ag6425/Ag6428/Ag6431/Ag6435/Ag6439/Ag6447 Seven experiments with different probe and primer sets are in excellent agreement. Highest

25   expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-34.5). Therefore, therapeutic modulation of this gene or the design of therapeutics with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting

30   and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a

functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

5   Low levels of expression of this gene is also seen in liver cirrhosis. Therefore, antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

           general oncology screening panel_v_2.4 Summary: Ag4983/Ag6442 Two experiments with different probe and primer sets are in excellent agreement. Highest
10   expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

           Moderate expression of this gene is seen in both normal and cancer samples derived from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this
15   gene seems to be higher in kidney and lung cancers as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

20   **AZ. CG56054-19: Integrin alpha 7-like protein.**

           Expression of gene CG56054-19 was assessed using the primer-probe sets Ag6442, Ag6424, Ag6425, Ag6428, Ag6430, Ag6431, Ag6439, Ag6440, Ag6391 and Ag6964, described in Tables AZA, AZB, AZC, AZD, AZE, AZF, AZG, AZH, AZI and AZJ. Results of the RTQ-PCR runs are shown in Tables AZK, AZL, AZM, AZN and AZO.

25   Table AZA. Probe Name Ag6442

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gatgtggacagtagggatagga-3'	22	1951	738
Probe	TET-5'-ccacctgagcagcaggagcct-3'-TAMRA	21	1990	739
Reverse	5'-gcgcagtccagggtg-3'	15	2076	740

Table AZB. Probe Name Ag6424

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ttgggttctgccagca-3'	16	641	741
Probe	TET-5'-cacagctgccgccttctccc-3'-TAMRA	20	660	742
Reverse	5'-aaaagcaaccccttccaa-3'	18	723	743

Table AZC. Probe Name Ag6425

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cggatgcacacccat-3'	16	2573	744
Probe	TET-5'-catcccgagctgggcccc-3'-TAMRA	18	2605	745
Reverse	5'-gccctggatgcccat-3'	15	2624	746

Table AZD. Probe Name Ag6428

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cttcatctaccatgggagca-3'	20	1293	747
Probe	TET-5'-ccttcacaggtgctggagggc-3'-TAMRA	21	1333	748
Reverse	5'-agggagtagccgaagctct-3'	19	1370	749

Table AZE. Probe Name Ag6430

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-gtgaccaacattgatagctcaga-3'	23	742	750
Probe	TET-5'-ccccgaccagctggtgtataaaactttg-3'-TAMRA	28	765	751
Reverse	5'-gggagccggtcagca-3'	15	798	752

5

Table AZF. Probe Name Ag6431

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaacatcaccctggactgc-3'	19	2070	753
Probe	TET-5'-tggtgttcagctgcccactctacag-3'-TAMRA	25	2111	754
Reverse	5'-ccgcgcggtcaaa-3'	13	2137	755

Table AZG. Probe Name Ag6439

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctgtggtggcagaaggagt-3'	19	2327	756
Probe	TET-5'-ccctggtgggtcatcctcctg-3'-TAMRA	21	2347	757
Reverse	5'-gaagaatcccatcttccacag-3'	21	2413	758

Table AZH. Probe Name Ag6440

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-accatcctgaggaacaactg-3'	20	2530	759
Probe	TET-5'-ctgacgggcatcccgagct-3'-TAMRA	19	2597	760
Reverse	5'-ccctggatgcccatc-3'	15	2623	761

Table AZI. Probe Name Ag6391

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tgcctccagggcctg-3'	15	1892	762
Probe	TET-5'-ctcccaggcccaacatcctcca-3'-TAMRA	22	1925	763
Reverse	5'-cgcctcctatccctactgtc-3'	20	1957	764

5   Table AZJ. Probe Name Ag6964

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ggccccagacatgca-3'	15	2156	765

Probe	TET-5'-actctacagctttgaccgcgcgg-3'-TAMRA	23	2127	766
Reverse	5'-gccaactgtgtggtgttca-3'	19	2101	767

Table AZK. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6425, Run 266937076	Rel. Exp.(%) Ag6428, Run 266937081	Rel. Exp.(%) Ag6430, Run 266937085	Rel. Exp.(%) Ag6431, Run 268030722	Rel. Exp.(%) Ag6439, Run 269254002	Rel. Exp.(%) Ag6440, Run 269254003	Rel. Exp.(%) Ag6442, Run 264979298
AD 1 Hippo	24.1	18.0	20.0	18.8	21.6	18.9	19.2
AD 2 Hippo	48.0	32.3	48.0	28.7	28.9	61.1	49.7
AD 3 Hippo	6.5	3.7	11.6	7.5	6.1	9.7	20.4
AD 4 Hippo	13.8	10.7	17.1	18.8	17.6	23.3	5.6
AD 5 Hippo	52.9	53.2	39.2	38.4	42.6	34.6	57.4
AD 6 Hippo	100.0	100.0	100.0	100.0	100.0	100.0	90.1
Control 2 Hippo	10.6	18.7	17.9	29.5	32.5	29.9	28.5
Control 4 Hippo	51.8	27.0	38.4	32.3	37.9	54.7	86.5
Control (Path) 3 Hippo	9.8	4.6	10.2	6.0	6.4	5.8	0.0
AD 1 Temporal Ctx	10.1	12.9	12.1	17.1	24.5	12.6	16.8
AD 2 Temporal Ctx	33.7	31.0	36.6	39.8	27.5	59.0	21.6
AD 3 Temporal Ctx	0.0	6.0	11.7	11.3	9.0	17.1	5.7
AD 4 Temporal Ctx	12.8	20.2	15.6	25.3	30.4	29.9	8.7
AD 5 Inf Temporal Ctx	59.0	39.2	43.8	36.3	41.8	41.8	73.7

AD 5 Sup Temporal Ctx	21.9	42.0	56.6	32.3	38.7	39.2	55.9
AD 6 Inf Temporal Ctx	73.7	49.3	40.9	46.7	47.6	48.6	76.8
AD 6 Sup Temporal Ctx	50.3	48.3	44.1	50.3	50.3	17.0	59.9
Control 1 Temporal Ctx	11.9	12.9	11.9	15.6	24.0	23.3	46.7
Control 2 Temporal Ctx	18.6	18.2	16.7	17.4	14.9	43.5	50.0
Control 3 Temporal Ctx	6.0	9.6	13.0	14.5	16.5	9.2	9.5
Control 3 Temporal Ctx	25.7	15.2	18.9	13.1	23.8	30.1	13.6
Control (Path) 1 Temporal Ctx	18.0	27.0	32.5	30.6	39.8	51.1	46.0
Control (Path) 2 Temporal Ctx	18.4	16.0	19.5	20.4	24.8	7.2	0.0
Control (Path) 3 Temporal Ctx	5.6	7.5	12.9	10.9	11.9	9.9	31.0
Control (Path) 4 Temporal Ctx	16.8	17.1	19.8	18.2	21.6	14.9	39.5
AD 1 Occipital Ctx	11.9	10.2	16.2	11.5	16.0	5.8	6.3
AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AD 3 Occipital Ctx	8.3	6.4	11.7	8.8	10.2	7.8	4.9

AD 4 Occipital Ctx	5.8	13.0	12.6	17.9	18.6	35.4	11.1
AD 5 Occipital Ctx	25.2	25.3	16.7	22.5	22.7	16.6	42.3
AD 6 Occipital Ctx	19.8	20.2	17.8	17.0	22.1	23.5	14.8
Control 1 Occipital Ctx	6.6	6.0	11.3	8.7	7.2	15.2	8.8
Control 2 Occipital Ctx	15.7	26.4	24.8	33.2	29.3	35.8	82.4
Control 3 Occipital Ctx	5.7	10.7	16.4	17.1	19.2	4.4	8.8
Control 4 Occipital Ctx	21.6	12.0	12.1	12.6	13.6	12.9	24.0
Control (Path) 1 Occipital Ctx	28.3	35.6	32.8	36.1	39.5	22.4	100.0
Control (Path) 2 Occipital Ctx	49.7	6.7	9.6	7.9	7.0	5.0	9.3
Control (Path) 3 Occipital Ctx	0.0	5.4	8.4	6.0	5.9	6.7	4.1
Control (Path) 4 Occipital Ctx	6.6	13.2	15.9	10.2	11.4	11.9	32.8
Control 1 Parietal Ctx	8.8	8.8	15.2	16.3	15.7	33.2	9.2
Control 2 Parietal Ctx	14.5	34.4	39.5	28.3	37.1	17.4	28.1
Control 3 Parietal Ctx	19.9	11.5	14.5	8.7	10.8	21.6	9.1
Control (Path) 1 Parietal Ctx	37.6	34.2	33.4	39.2	37.9	47.3	69.3
Control (Path) 2 Parietal Ctx	16.6	19.6	20.0	22.5	18.7	17.1	37.6
Control (Path) 3 Parietal Ctx	0.0	3.9	15.0	7.1	12.0	11.7	10.4

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Control (Path) 4 Parietal Ctx	18.2	24.8	28.3	8.8	27.9	29.3	27.5

Table AZL. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979530
Adipose	3.2	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.5	Bladder	2.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	0.7	Gastric ca. KATO III	0.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.1
Melanoma* SK-MEL-5	8.9	Colon ca. SW480	17.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	7.9
Testis Pool	3.5	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.1	Colon ca. HCT-116	2.4
Prostate Pool	3.1	Colon ca. CaCo-2	10.2
Placenta	0.4	Colon cancer tissue	10.7
Uterus Pool	5.4	Colon ca. SW1116	1.3
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.7
Ovarian ca. OVCAR-4	0.3	Colon Pool	6.3
Ovarian ca. OVCAR-5	0.8	Small Intestine Pool	5.2
Ovarian ca. IGROV-1	66.0	Stomach Pool	4.3
Ovarian ca. OVCAR-8	11.2	Bone Marrow Pool	3.3
Ovary	2.0	Fetal Heart	7.6
Breast ca. MCF-7	0.1	Heart Pool	13.3
Breast ca. MDA-MB-231	0.2	Lymph Node Pool	7.1
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	16.5
Breast ca. T47D	0.0	Skeletal Muscle Pool	100.0
Breast ca. MDA-N	0.5	Spleen Pool	1.9

Breast Pool	7.4	Thymus Pool	5.5
Trachea	2.4	CNS cancer (glio/astro) U87-MG	7.4
Lung	3.5	CNS cancer (glio/astro) U-118-MG	2.6
Fetal Lung	3.8	CNS cancer (neuro;met) SK-N-AS	1.2
Lung ca. NCI-N417	1.6	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	1.4	CNS cancer (astro) SNB-75	6.7
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	63.7
Lung ca. SHP-77	2.0	CNS cancer (glio) SF-295	4.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	5.0
Lung ca. NCI-H526	0.6	Brain (cerebellum)	3.3
Lung ca. NCI-H23	2.0	Brain (fetal)	1.9
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	5.7
Lung ca. HOP-62	0.6	Cerebral Cortex Pool	4.6
Lung ca. NCI-H522	1.1	Brain (Substantia nigra) Pool	5.1
Liver	0.2	Brain (Thalamus) Pool	3.7
Fetal Liver	0.2	Brain (whole)	3.2
Liver ca. HepG2	0.0	Spinal Cord Pool	9.0
Kidney Pool	15.6	Adrenal Gland	3.1
Fetal Kidney	1.0	Pituitary gland Pool	0.7
Renal ca. 786-0	0.2	Salivary Gland	0.7
Renal ca. A498	0.2	Thyroid (female)	1.0
Renal ca. ACHN	0.2	Pancreatic ca. CAPAN2	0.5
Renal ca. UO-31	0.4	Pancreas Pool	8.8

Table AZM. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6424, Run 277221719	Rel. Exp.(%) Ag6425, Run 277221721	Rel. Exp.(%) Ag6428, Run 277222439	Rel. Exp.(%) Ag6430, Run 277222443	Rel. Exp.(%) Ag6431, Run 277633568	Rel. Exp.(%) Ag6431, Run 278389390	Rel. Exp.(%) Ag6439, Run 277223175	Rel. Exp.(%) Ag6440, Run 277223177	Rel. Exp.(%) Ag6964, Run 278388946
Adipose	0.0	2.6	20.0	8.2	17.4	13.8	17.3	3.7	18.8
Melanoma* Hs688(A).T	0.0	0.0	2.0	0.5	0.8	0.9	0.4	0.0	0.7
Melanoma* Hs688(B).T	0.0	0.2	4.1	0.6	2.5	2.2	2.9	0.8	2.4
Melanoma* M14	0.0	0.0	0.7	0.7	0.4	0.4	0.4	0.0	0.7
Melanoma* LOXIMVI	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.1
Melanoma* SK-MEL-5	0.0	2.2	30.4	22.5	18.2	14.6	18.3	3.0	15.9
Squamous cell carcinoma SCC-4	0.0	0.0	0.1	0.3	0.1	0.2	0.0	0.0	0.1
Testis Pool	0.0	3.5	8.8	4.2	10.4	9.0	9.1	3.0	9.9
Prostate ca.* (bone met) PC-3	0.0	0.5	2.5	1.0	1.9	1.8	1.3	1.2	4.3
Prostate Pool	0.0	1.0	11.5	8.5	11.3	12.1	28.5	2.1	10.0
Placenta	0.0	0.0	0.7	0.1	0.1	0.1	0.5	0.0	0.4
Uterus Pool	0.0	1.5	4.5	2.6	4.6	4.5	5.3	2.3	4.1
Ovarian ca. OVCAR-3	0.0	0.3	1.1	0.8	0.7	1.1	1.6	0.4	4.0
Ovarian ca. SK-OV-3	0.0	0.2	1.7	1.5	0.8	0.9	1.3	0.5	1.7
Ovarian ca. OVCAR-4	0.0	0.0	0.9	0.5	0.4	0.8	0.9	0.0	0.5
Ovarian ca. OVCAR-5	0.0	1.3	2.9	1.5	1.3	1.7	1.4	4.2	7.9
Ovarian ca. IGROV-1	100.0	100.0	77.9	90.8	84.7	97.9	69.3	100.0	75.8

Ovarian ca. OVCAR-8	5.6	21.9	14.0	11.9	15.6	14.6	17.3	18.2	16.7
Ovary	0.0	0.3	5.2	2.1	3.1	2.3	2.8	0.8	2.4
Breast ca. MCF-7	0.0	0.0	0.3	0.4	0.1	0.2	0.5	0.3	0.5
Breast ca. MDA-MB-231	0.0	0.0	0.4	0.4	0.2	0.2	0.2	0.0	0.3
Breast ca. BT 549	0.0	0.0	0.5	0.3	0.1	0.5	0.6	0.0	0.4
Breast ca. T47D	0.0	0.0	0.5	0.3	0.2	0.3	0.4	0.3	0.5
Breast ca. MDA-N	0.0	0.0	0.7	0.7	0.6	0.6	0.6	0.3	0.8
Breast Pool	0.0	4.1	21.8	19.5	14.6	10.7	12.2	3.5	16.7
Trachea	0.0	0.7	8.4	2.9	4.8	4.2	4.7	1.4	5.6
Lung	0.0	0.7	2.3	1.3	4.2	3.2	3.9	5.3	5.1
Fetal Lung	0.0	0.3	9.1	4.0	5.0	4.8	5.3	2.9	6.1
Lung ca. NCI-N417	2.0	0.9	3.5	2.7	3.3	2.6	4.0	2.0	2.3
Lung ca. LX-1	3.1	2.7	6.5	7.0	5.0	3.5	4.9	6.3	44.1
Lung ca. NCI-H146	0.0	0.0	0.3	0.5	0.1	0.2	0.1	0.0	0.1
Lung ca. SHP-77	2.3	0.4	6.8	6.3	5.3	4.5	4.5	0.8	3.8
Lung ca. A549	0.0	2.6	0.9	0.3	0.0	0.4	0.6	2.2	4.7
Lung ca. NCI-H526	0.0	0.0	0.9	0.7	0.6	0.3	0.4	0.3	0.5
Lung ca. NCI-H23	0.0	1.0	4.6	4.5	4.8	3.2	2.9	2.3	10.3
Lung ca. NCI-H460	0.0	0.0	0.2	0.2	0.1	0.3	0.0	0.0	0.3
Lung ca. HOP-62	0.0	0.0	0.5	0.6	1.0	0.6	0.5	0.0	0.7
Lung ca. NCI-H522	0.0	0.6	2.3	2.4	1.7	1.3	3.3	2.5	8.9

Liver	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.4	2.0
Fetal Liver	0.0	0.3	1.1	0.6	0.6	0.5	0.8	0.8	8.2
Liver ca. HepG2	0.0	0.3	0.2	0.1	0.0	0.2	0.1	0.9	2.4
Kidney Pool	6.5	0.0	47.0	34.9	33.9	28.1	43.2	14.6	32.8
Fetal Kidney	0.0	0.0	4.9	5.1	4.1	4.0	5.8	3.4	11.5
Renal ca. 786-0	0.0	0.0	0.2	0.2	0.3	0.1	0.3	0.0	0.9
Renal ca. A498	0.0	1.8	0.2	0.1	0.0	0.3	0.5	3.8	8.5
Renal ca. ACHN	0.0	0.5	2.5	0.7	1.7	1.5	1.2	0.5	2.5
Renal ca. UO-31	0.0	0.0	0.5	0.3	0.2	0.2	0.6	0.0	0.3
Renal ca. TK-10	0.0	0.4	3.1	2.5	2.0	1.9	2.1	0.5	4.6
Bladder	0.0	0.0	5.9	3.0	5.5	5.1	8.3	0.9	6.7
Gastric ca. (liver met.) NCI-N87	0.0	0.0	1.7	1.7	0.9	1.2	1.1	0.8	6.7
Gastric ca. KATO III	0.0	0.5	0.8	0.4	0.2	0.3	0.4	0.4	0.9
Colon ca. SW-948	0.0	1.5	0.2	0.0	0.2	0.2	0.3	2.2	1.2
Colon ca. SW480	9.5	5.2	41.8	39.0	27.0	23.3	23.0	6.3	33.7
Colon ca.* (SW480 met) SW620	7.7	4.8	16.4	15.5	12.8	10.3	6.1	7.2	25.0
Colon ca. HT29	0.0	0.0	0.0	0.0	0.2	0.2	0.0	0.3	0.3
Colon ca. HCT-116	1.6	0.2	3.2	3.8	2.5	2.0	2.1	0.6	4.3
Colon ca. CaCo-2	10.4	3.6	27.0	22.2	19.1	16.7	18.3	6.5	38.2
Colon cancer tissue	0.0	3.3	11.0	6.5	11.9	7.6	7.7	4.4	20.4
Colon ca. SW1116	0.0	3.0	2.5	1.7	2.0	1.5	1.8	2.1	6.0

Colon ca. Colo-205	0.0	0.4	0.3	0.2	0.2	0.0	0.2	1.3	0.8
Colon ca. SW-48	0.0	3.6	1.4	1.3	1.5	1.5	1.4	3.0	2.6
Colon Pool	0.0	5.0	28.1	28.7	23.2	18.7	25.5	8.1	20.6
Small Intestine Pool	0.0	1.7	17.1	10.5	11.2	13.0	12.8	2.0	10.4
Stomach Pool	0.0	2.3	14.3	6.2	9.5	9.3	8.5	4.2	10.7
Bone Marrow Pool	0.0	1.6	14.3	11.3	10.2	8.7	18.7	3.5	12.5
Fetal Heart	0.0	2.3	25.5	24.3	24.5	21.8	33.7	8.6	20.7
Heart Pool	5.2	7.0	29.7	23.0	25.9	17.2	33.7	10.7	26.1
Lymph Node Pool	0.0	6.1	33.7	30.4	22.1	23.7	19.9	6.7	24.7
Fetal Skeletal Muscle	36.9	5.2	54.3	46.7	48.6	46.3	19.1	19.2	50.7
Skeletal Muscle Pool	12.3	9.2	29.3	21.5	29.5	25.9	22.1	22.7	32.3
Spleen Pool	0.0	0.0	1.9	2.0	2.0	1.7	2.7	0.6	3.1
Thymus Pool	0.0	2.0	10.4	7.5	8.1	9.4	7.7	3.1	7.0
CNS cancer (glio/astro) U87-MG	1.6	1.5	14.9	6.1	10.7	10.0	10.9	2.2	14.1
CNS cancer (glio/astro) U-118-MG	0.0	0.3	4.7	2.9	3.8	3.1	3.8	0.8	5.8
CNS cancer (neuro;met) SK-N-AS	0.0	0.0	2.6	1.7	2.1	1.0	1.4	0.5	2.6
CNS cancer (astro) SF-539	0.0	0.0	0.0	0.2	0.1	0.2	0.1	0.2	0.1
CNS cancer (astro) SNB-75	1.9	1.1	14.9	5.9	6.5	10.0	11.7	2.8	9.7

CNS cancer (glio) SNB-19	84.1	79.0	100.0	100.0	100.0	100.0	100.0	97.9	100.0
CNS cancer (glio) SF-295	1.8	0.0	11.3	9.0	8.0	7.8	8.2	1.5	14.8
Brain (Amygdala) Pool	2.3	0.8	7.7	6.9	6.2	4.8	8.0	4.4	5.3
Brain (cerebellum)	6.6	0.4	19.8	11.1	10.7	9.7	8.8	1.2	9.7
Brain (fetal)	3.0	0.7	12.7	11.5	6.6	5.6	6.8	2.1	6.4
Brain (Hippocampus) Pool	3.1	3.2	11.7	11.0	8.6	6.9	11.0	4.3	10.2
Cerebral Cortex Pool	1.7	0.6	11.0	7.5	7.5	0.7	11.6	2.0	8.7
Brain (Substantia nigra) Pool	1.8	2.2	11.7	8.5	10.4	4.7	10.0	2.0	9.3
Brain (Thalamus) Pool	0.0	2.7	13.2	10.0	9.3	0.2	9.7	2.8	8.7
Brain (whole)	0.0	0.4	10.6	8.0	5.8	0.3	5.6	1.9	8.7
Spinal Cord Pool	3.2	2.3	14.7	12.8	11.0	7.6	12.2	4.2	9.0
Adrenal Gland	0.0	0.3	9.9	6.1	3.9	3.7	4.8	0.9	4.1
Pituitary gland Pool	0.0	0.0	1.1	0.8	1.2	1.1	1.4	0.6	0.5
Salivary Gland	0.0	0.0	1.8	1.1	1.3	0.9	1.1	0.0	1.0
Thyroid (female)	0.0	0.3	3.1	0.8	2.5	2.5	1.9	1.3	2.3
Pancreatic ca. CAPAN2	0.0	0.0	0.8	0.8	0.7	0.6	0.7	0.6	2.2
Pancreas Pool	0.0	0.0	2.0	1.1	1.1	1.6	3.2	1.0	2.3

Table AZN. Panel 4.1D

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Tissue Name	Rel. Exp.(%) Ag6425, Run 268713999	Rel. Exp.(%) Ag6428, Run 268767535	Rel. Exp.(%) Ag6430, Run 268767563	Rel. Exp.(%) Ag6431, Run 268767577	Rel. Exp.(%) Ag6439, Run 268760823	Rel. Exp.(%) Ag6440, Run 268760825
Secondary Th1 act	0.0	1.3	0.0	0.7	0.0	0.0
Secondary Th2 act	0.0	1.2	0.0	0.8	0.0	0.0
Secondary Tr1 act	0.0	0.0	0.0	0.7	0.0	0.0
Secondary Th1 rest	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Th2 rest	0.0	0.0	0.0	0.0	0.0	0.0
Secondary Tr1 rest	0.0	0.4	0.0	0.0	0.0	0.0
Primary Th1 act	0.0	0.0	0.0	0.0	0.0	0.0
Primary Th2 act	0.0	0.3	0.0	0.4	0.0	0.0
Primary Tr1 act	0.0	0.7	0.0	0.7	0.0	0.0
Primary Th1 rest	0.0	0.1	0.0	0.3	1.2	0.0
Primary Th2 rest	0.0	0.4	0.0	0.2	0.0	0.0
Primary Tr1 rest	0.0	0.0	0.0	0.0	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	5.4	0.0	2.4	2.6	0.0
CD45RO CD4 lymphocyte act	0.0	1.5	0.0	0.7	2.3	0.0
CD8 lymphocyte act	0.0	0.7	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	8.8	0.0	0.0	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.4	0.0	0.3	0.0	0.0
CD4 lymphocyte none	0.0	0.5	0.0	0.4	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	0.0	0.0	0.0	1.2	0.0
LAK cells rest	2.7	11.8	0.1	3.8	15.2	0.0
LAK cells IL-2	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	0.0	0.0	0.0	0.0

LAK cells IL-2+IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	0.0	0.0	0.0	0.0
LAK cells PMA/ionomycin	15.7	15.1	0.1	6.3	9.0	52.9
NK Cells IL-2 rest	0.0	3.4	0.0	2.5	1.4	0.0
Two Way MLR 3 day	0.0	2.2	0.0	1.3	1.4	0.0
Two Way MLR 5 day	0.0	0.8	0.0	0.9	0.0	0.0
Two Way MLR 7 day	13.2	1.1	0.0	2.6	3.7	0.0
PBMC rest	0.0	0.0	0.0	0.0	0.0	0.0
PBMC PWM	0.0	1.3	0.0	0.0	0.0	0.0
PBMC PHA-L	0.0	0.6	0.0	0.7	0.0	0.0
Ramos (B cell) none	0.0	0.0	0.0	0.0	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.7	0.0	0.2	0.0	0.0
B lymphocytes PWM	0.0	0.0	0.0	0.0	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.9	0.0	0.0	0.0	0.0
EOL-1 dbcAMP	9.1	29.1	0.1	8.1	68.8	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	0.0	2.7	1.8	0.0
Dendritic cells none	13.8	4.1	0.0	5.3	0.0	0.0
Dendritic cells LPS	0.0	1.0	0.0	0.7	0.0	0.0
Dendritic cells anti-CD40	3.3	0.5	0.0	0.2	0.0	0.0
Monocytes rest	0.0	0.4	0.0	0.0	0.0	0.0
Monocytes LPS	0.0	5.7	0.0	1.8	2.6	0.0
Macrophages rest	0.0	0.6	0.0	0.6	0.0	0.0
Macrophages LPS	0.0	5.4	0.1	6.3	9.2	0.0
HUVEC none	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC starved	0.0	0.0	0.0	0.3	0.0	0.0

HUVEC IL-1beta	0.0	0.0	0.0	0.5	0.0	0.0
HUVEC IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IFN gamma	0.0	0.0	0.0	0.0	0.0	0.0
HUVEC TNF alpha + IL4	0.0	0.0	0.0	0.4	0.0	0.0
HUVEC IL-11	0.0	0.4	0.0	0.3	0.0	0.0
Lung Microvascular EC none	0.0	0.4	0.0	0.0	0.0	0.0
Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0	0.0	0.0
Microvascular Dermal EC none	0.0	0.0	0.0	0.0	0.0	0.0
Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0	0.0	0.0	0.0	0.0
Bronchial epithelium TNFalpha + IL1beta	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium none	0.0	0.0	0.0	0.0	0.0	0.0
Small airway epithelium TNFalpha + IL-1beta	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC rest	0.0	0.0	0.0	0.0	0.0	0.0
Coronery artery SMC TNFalpha + IL-1beta	6.2	0.3	0.0	1.5	0.0	0.0
Astrocytes rest	100.0	100.0	12.0	100.0	100.0	100.0
Astrocytes TNFalpha + IL-1beta	74.2	97.3	100.0	74.7	95.9	95.3
KU-812 (Basophil) rest	0.0	0.0	0.0	0.4	0.0	0.0
KU-812 (Basophil) PMA/ionomycin	0.0	0.0	0.0	0.0	0.0	0.0

CCD1106 (Keratinocytes) none	0.0	0.0	0.0	0.8	0.0	0.0
CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0	0.0	0.0	0.0	0.0
Liver cirrhosis	4.6	2.6	0.0	6.7	8.5	0.0
NCI-H292 none	0.0	1.7	0.0	0.6	0.0	0.0
NCI-H292 IL-4	0.0	0.0	0.0	0.5	0.0	0.0
NCI-H292 IL-9	0.0	0.7	0.0	0.5	0.0	0.0
NCI-H292 IL-13	0.0	0.9	0.0	0.9	0.0	0.0
NCI-H292 IFN gamma	0.0	0.5	0.0	0.6	0.0	0.0
HPAEC none	0.0	0.0	0.0	0.0	0.0	0.0
HPAEC TNF alpha + IL-1 beta	0.0	0.0	0.0	0.0	0.0	0.0
Lung fibroblast none	31.4	95.9	0.2	65.5	94.0	54.3
Lung fibroblast TNF alpha + IL-1 beta	22.2	48.6	0.1	39.8	62.9	52.5
Lung fibroblast IL-4	19.1	27.4	0.1	21.2	34.9	0.0
Lung fibroblast IL-9	23.5	24.0	0.1	26.8	96.6	66.0
Lung fibroblast IL-13	4.5	11.9	0.0	10.4	13.4	0.0
Lung fibroblast IFN gamma	15.7	55.9	0.2	46.3	89.5	47.0
Dermal fibroblast CCD1070 rest	0.0	6.0	0.0	6.3	4.1	0.0
Dermal fibroblast CCD1070 TNF alpha	0.0	2.7	0.0	0.8	2.3	0.0
Dermal fibroblast CCD1070 IL-1 beta	0.0	5.6	0.0	1.3	0.0	0.0
Dermal fibroblast IFN gamma	8.5	30.6	0.1	20.2	26.6	0.0
Dermal fibroblast IL-4	4.1	30.8	0.1	19.8	25.5	0.0
Dermal Fibroblasts rest	8.0	54.3	0.1	46.7	47.3	0.0

Neutrophils TNFa+LPS	0.0	0.9	0.0	0.4	0.0	0.0
Neutrophils rest	0.0	0.0	0.0	0.3	0.0	0.0
Colon	4.0	4.6	0.0	9.5	8.4	0.0
Lung	0.0	2.8	0.0	4.6	2.1	0.0
Thymus	0.0	0.0	0.0	0.4	2.4	0.0
Kidney	4.9	7.8	0.1	9.7	5.2	0.0

Table AZO. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag6442, Run 264979180	Tissue Name	Rel. Exp.(%) Ag6442, Run 264979180
Colon cancer 1	22.7	Bladder cancer NAT 2	1.4
Colon cancer NAT 1	**100.0**	Bladder cancer NAT 3	4.8
Colon cancer 2	0.0	Bladder cancer NAT 4	66.0
Colon cancer NAT 2	15.1	Prostate adenocarcinoma 1	7.5
Colon cancer 3	2.8	Prostate adenocarcinoma 2	8.0
Colon cancer NAT 3	40.1	Prostate adenocarcinoma 3	9.0
Colon malignant cancer 4	9.5	Prostate adenocarcinoma 4	9.1
Colon normal adjacent tissue 4	0.9	Prostate cancer NAT 5	9.9
Lung cancer 1	6.6	Prostate adenocarcinoma 6	7.7
Lung NAT 1	0.0	Prostate adenocarcinoma 7	17.3
Lung cancer 2	15.9	Prostate adenocarcinoma 8	0.0
Lung NAT 2	0.0	Prostate adenocarcinoma 9	33.9
Squamous cell carcinoma 3	8.3	Prostate cancer NAT 10	4.9
Lung NAT 3	0.0	Kidney cancer 1	16.5
metastatic melanoma 1	49.0	KidneyNAT 1	7.2

Melanoma 2	1.1	Kidney cancer 2	73.7
Melanoma 3	13.8	Kidney NAT 2	19.2
metastatic melanoma 4	24.0	Kidney cancer 3	21.3
metastatic melanoma 5	31.4	Kidney NAT 3	11.4
Bladder cancer 1	2.1	Kidney cancer 4	25.7
Bladder cancer NAT 1	0.0	Kidney NAT 4	14.9
Bladder cancer 2	19.3		

CNS_neurodegeneration_v1.0

Summary: Ag6425/Ag6428/Ag6430/Ag6431/Ag6439/ Ag6440/Ag6442 Seven experiments with different probe and primer sets are in excellent agreement. This panel confirms the expression of this gene at low levels in the brains of an independent group of

5   individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. See Panel 1.4 for a discussion of this gene in treatment of central nervous system disorders.

Ag6424/Ag6391 Expression of this gene is low/undetectable (CTs > 35) across all

10   of the samples on this panel (data not shown).

General_screening_panel_v1.5 Summary: Ag6442 Highest expression of this gene is seen in skeletal muscle (CT=28). Expression of this gene is higher in adult (CT=28) as compared to the fetal skeletal muscle (CT=31). Therefore, expression of this gene may be used to distinguish fetal from adult skeletal muscle.

15   In addition moderate to low levels of expression of this gene is also seen in all the regions of central nervous system, in tissues with metabolic/endocrine functions and in a number of cancer cell lines derived from melanoma, brain, colon, lung, and ovarian cancers. This expression pattern is consistent with the expression seen in panel 1.4. See panel 1.4 for further discussion on the utility of these genes.

20   **General_screening_panel_v1.6 Summary:** Ag6424/ Ag6425/Ag6428/Ag6430/Ag6431/Ag6439/Ag6440/Ag6964 Nine experiments with seven different probe and primer sets are in very good agreement. Highest expression of this gene is detected in a ovarian cancer IGROV-1 cell line and brain cancer SNB-19 cell lines (CTs=25-33.7). In addition, consistent with expression seen in panel 1.4, moderate to low

levels of expression of this gene is also seen in all the regions of central nervous system, tissues with metabolic/endocrine functions, and number of cancer cell lines. See panel 1.4 for further discussion of this gene.

Ag6391 Expression of this gene is low/undetectable (CTs > 35) across all of the
5   samples on this panel (data not shown).

Panel 4.1D Summary: Ag6425/Ag6428/Ag6430/Ag6431/Ag6439/ Ag6440 Seven experiments with different probe and primer sets are in excellent agreement. Highest expression of this gene is detected in both resting and cytokine activated astrocytes (CTs=22-33.5). Therefore, therapeutic modulation of this gene or the design of therapeutics
10   with the encoded protein could be important in the treatment of multiple sclerosis or other inflammatory diseases of the CNS.

In addition, moderate to low levels of expression of this gene is also seen in resting and cytokine treated lung and dermal fibroblasts, as well as in normal tissues represented by colon, lung, thymus and kidney. Therefore, modulation of the gene product with a
15   functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Low levels of expression of this gene is also seen in liver cirrhosis. Therefore,
20   antibodies or small molecule therapeutics could reduce or inhibit fibrosis that occurs in liver cirrhosis.

Ag6424 Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

general oncology screening panel_v_2.4 Summary: Ag6442 Two experiments
25   with different probe and primer sets are in excellent agreement. Highest expression of this gene is seen in normal colon (CTs=29-32). Expression of this gene in normal colon is higher than in the corresponding cancer samples (CTs=32-34). Therefore, expression of this gene may be used to distinguish between these two samples.

Moderate expression of this gene is seen in both normal and cancer samples derived
30   from colon, lung, bladder, prostate and kidney, as well as, in melanomas. Expression of this gene seems to be higher in kidney and lung cancers as compared to the corresponding

normal adjacent samples. Therefore, expression of this gene may be used as marker to detect the presence of lung and kidney cancers. Furthermore, therapeutic modulation of this gene may be useful in the treatment of melanoma, colon, lung, bladder, prostate and kidney cancers.

5   **BA. CG88634-01: KIAA1219-like protein.**

Expression of gene CG88634-01 was assessed using the primer-probe set Ag3649, described in Table BAA. Results of the RTQ-PCR runs are shown in Tables BAB, BAC, BAD and BAE.

Table BAA. Probe Name Ag3649

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ccgcaagaattgaatcagtatc-3'	22	1055	768
Probe	TET-5'-cctgccttaaacatctgcctcaaata-3'-TAMRA	26	1077	769
Reverse	5'-catccaccagacagctgatt-3'	20	1123	770

10   Table BAB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3649, Run 211019464	Tissue Name	Rel. Exp.(%) Ag3649, Run 211019464
AD 1 Hippo	12.1	Control (Path) 3 Temporal Ctx	4.5
AD 2 Hippo	28.3	Control (Path) 4 Temporal Ctx	40.9
AD 3 Hippo	6.7	AD 1 Occipital Ctx	12.2
AD 4 Hippo	7.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	6.7
AD 6 Hippo	47.6	AD 4 Occipital Ctx	24.7
Control 2 Hippo	25.2	AD 5 Occipital Ctx	20.0
Control 4 Hippo	9.2	AD 6 Occipital Ctx	46.3
Control (Path) 3 Hippo	7.5	Control 1 Occipital Ctx	6.7
AD 1 Temporal Ctx	18.6	Control 2 Occipital Ctx	52.1

AD 2 Temporal Ctx	30.4	Control 3 Occipital Ctx	17.0
AD 3 Temporal Ctx	5.9	Control 4 Occipital Ctx	6.6
AD 4 Temporal Ctx	24.5	Control (Path) 1 Occipital Ctx	73.2
AD 5 Inf Temporal Ctx	92.0	Control (Path) 2 Occipital Ctx	10.9
AD 5 SupTemporal Ctx	48.0	Control (Path) 3 Occipital Ctx	3.3
AD 6 Inf Temporal Ctx	51.4	Control (Path) 4 Occipital Ctx	18.4
AD 6 Sup Temporal Ctx	47.6	Control 1 Parietal Ctx	5.3
Control 1 Temporal Ctx	6.9	Control 2 Parietal Ctx	41.5
Control 2 Temporal Ctx	28.1	Control 3 Parietal Ctx	17.3
Control 3 Temporal Ctx	12.9	Control (Path) 1 Parietal Ctx	65.1
Control 4 Temporal Ctx	6.9	Control (Path) 2 Parietal Ctx	24.8
Control (Path) 1 Temporal Ctx	57.0	Control (Path) 3 Parietal Ctx	5.3
Control (Path) 2 Temporal Ctx	36.3	Control (Path) 4 Parietal Ctx	49.0

Table BAC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3649, Run 219798089	Tissue Name	Rel. Exp.(%) Ag3649, Run 219798089
Adipose	14.5	Renal ca. TK-10	46.0
Melanoma* Hs688(A).T	31.9	Bladder	26.4
Melanoma* Hs688(B).T	25.9	Gastric ca. (liver met.) NCI-N87	99.3
Melanoma* M14	31.6	Gastric ca. KATO III	83.5
Melanoma* LOXIMVI	23.8	Colon ca. SW-948	5.9
Melanoma* SK-MEL-5	44.8	Colon ca. SW480	63.7
Squamous cell carcinoma SCC-4	15.6	Colon ca.* (SW480 met) SW620	41.2
Testis Pool	19.9	Colon ca. HT29	20.6

Prostate ca.* (bone met) PC-3	47.6	Colon ca. HCT-116	26.2
Prostate Pool	19.3	Colon ca. CaCo-2	87.1
Placenta	21.5	Colon cancer tissue	30.6
Uterus Pool	12.3	Colon ca. SW1116	7.9
Ovarian ca. OVCAR-3	73.7	Colon ca. Colo-205	7.0
Ovarian ca. SK-OV-3	51.8	Colon ca. SW-48	8.8
Ovarian ca. OVCAR-4	25.2	Colon Pool	28.3
Ovarian ca. OVCAR-5	44.1	Small Intestine Pool	22.2
Ovarian ca. IGROV-1	18.8	Stomach Pool	11.4
Ovarian ca. OVCAR-8	11.0	Bone Marrow Pool	16.0
Ovary	15.5	Fetal Heart	26.8
Breast ca. MCF-7	35.6	Heart Pool	14.0
Breast ca. MDA-MB-231	77.4	Lymph Node Pool	29.7
Breast ca. BT 549	89.5	Fetal Skeletal Muscle	14.2
Breast ca. T47D	85.9	Skeletal Muscle Pool	13.5
Breast ca. MDA-N	25.2	Spleen Pool	17.0
Breast Pool	27.0	Thymus Pool	25.0
Trachea	23.5	CNS cancer (glio/astro) U87-MG	62.0
Lung	5.7	CNS cancer (glio/astro) U-118-MG	76.3
Fetal Lung	51.4	CNS cancer (neuro;met) SK-N-AS	63.7
Lung ca. NCI-N417	5.1	CNS cancer (astro) SF-539	30.8
Lung ca. LX-1	45.4	CNS cancer (astro) SNB-75	**100.0**
Lung ca. NCI-H146	19.1	CNS cancer (glio) SNB-19	18.8
Lung ca. SHP-77	28.5	CNS cancer (glio) SF-295	84.1
Lung ca. A549	19.9	Brain (Amygdala) Pool	10.6
Lung ca. NCI-H526	12.0	Brain (cerebellum)	65.5
Lung ca. NCI-H23	64.6	Brain (fetal)	36.3

Lung ca. NCI-H460	19.2	Brain (Hippocampus) Pool	11.4
Lung ca. HOP-62	8.2	Cerebral Cortex Pool	19.9
Lung ca. NCI-H522	27.5	Brain (Substantia nigra) Pool	10.0
Liver	3.0	Brain (Thalamus) Pool	22.4
Fetal Liver	16.6	Brain (whole)	20.9
Liver ca. HepG2	27.0	Spinal Cord Pool	11.3
Kidney Pool	26.1	Adrenal Gland	25.3
Fetal Kidney	34.2	Pituitary gland Pool	11.2
Renal ca. 786-0	25.5	Salivary Gland	9.5
Renal ca. A498	12.7	Thyroid (female)	6.0
Renal ca. ACHN	21.9	Pancreatic ca. CAPAN2	33.4
Renal ca. UO-31	0.0	Pancreas Pool	28.1

Table BAD. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3649, Run 169975759	Tissue Name	Rel. Exp.(%) Ag3649, Run 169975759
Secondary Th1 act	57.4	HUVEC IL-1beta	55.5
Secondary Th2 act	67.8	HUVEC IFN gamma	66.4
Secondary Tr1 act	81.8	HUVEC TNF alpha + IFN gamma	50.0
Secondary Th1 rest	25.5	HUVEC TNF alpha + IL4	40.3
Secondary Th2 rest	47.6	HUVEC IL-11	32.3
Secondary Tr1 rest	41.8	Lung Microvascular EC none	96.6
Primary Th1 act	44.8	Lung Microvascular EC TNFalpha + IL-1beta	97.3
Primary Th2 act	54.3	Microvascular Dermal EC none	55.9
Primary Tr1 act	49.7	Microsvasular Dermal EC TNFalpha + IL-1beta	60.3
Primary Th1 rest	36.3	Bronchial epithelium TNFalpha + IL1beta	47.3
Primary Th2 rest	41.5	Small airway epithelium none	23.7

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Primary Tr1 rest	55.1	Small airway epithelium TNFalpha + IL-1beta	45.1
CD45RA CD4 lymphocyte act	38.4	Coronery artery SMC rest	33.7
CD45RO CD4 lymphocyte act	56.3	Coronery artery SMC TNFalpha + IL-1beta	40.1
CD8 lymphocyte act	50.0	Astrocytes rest	40.1
Secondary CD8 lymphocyte rest	51.4	Astrocytes TNFalpha + IL-1beta	29.9
Secondary CD8 lymphocyte act	29.9	KU-812 (Basophil) rest	27.7
CD4 lymphocyte none	42.0	KU-812 (Basophil) PMA/ionomycin	48.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	45.4	CCD1106 (Keratinocytes) none	79.0
LAK cells rest	48.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	100.0
LAK cells IL-2	54.7	Liver cirrhosis	17.2
LAK cells IL-2+IL-12	46.3	NCI-H292 none	41.5
LAK cells IL-2+IFN gamma	61.6	NCI-H292 IL-4	71.7
LAK cells IL-2+ IL-18	65.5	NCI-H292 IL-9	100.0
LAK cells PMA/ionomycin	46.0	NCI-H292 IL-13	75.3
NK Cells IL-2 rest	65.1	NCI-H292 IFN gamma	72.2
Two Way MLR 3 day	64.6	HPAEC none	43.8
Two Way MLR 5 day	45.1	HPAEC TNF alpha + IL-1 beta	92.0
Two Way MLR 7 day	30.4	Lung fibroblast none	56.3
PBMC rest	29.9	Lung fibroblast TNF alpha + IL-1 beta	27.9
PBMC PWM	31.2	Lung fibroblast IL-4	39.8
PBMC PHA-L	40.3	Lung fibroblast IL-9	53.6
Ramos (B cell) none	47.3	Lung fibroblast IL-13	31.4
Ramos (B cell) ionomycin	49.7	Lung fibroblast IFN gamma	42.9

B lymphocytes PWM	28.5	Dermal fibroblast CCD1070 rest	55.9
B lymphocytes CD40L and IL-4	55.1	Dermal fibroblast CCD1070 TNF alpha	83.5
EOL-1 dbcAMP	46.7	Dermal fibroblast CCD1070 IL-1 beta	36.1
EOL-1 dbcAMP PMA/ionomycin	66.0	Dermal fibroblast IFN gamma	34.9
Dendritic cells none	44.8	Dermal fibroblast IL-4	61.6
Dendritic cells LPS	36.6	Dermal Fibroblasts rest	37.1
Dendritic cells anti-CD40	53.2	Neutrophils TNFa+LPS	14.3
Monocytes rest	58.2	Neutrophils rest	64.6
Monocytes LPS	80.7	Colon	19.9
Macrophages rest	41.2	Lung	30.4
Macrophages LPS	28.7	Thymus	85.3
HUVEC none	28.9	Kidney	45.7
HUVEC starved	52.1		

Table BAE. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag3649, Run 267777885	Tissue Name	Rel. Exp.(%) Ag3649, Run 267777885
Colon cancer 1	30.4	Bladder cancer NAT 2	2.0
Colon cancer NAT 1	7.7	Bladder cancer NAT 3	4.8
Colon cancer 2	29.7	Bladder cancer NAT 4	14.8
Colon cancer NAT 2	10.7	Prostate adenocarcinoma 1	65.5
Colon cancer 3	76.3	Prostate adenocarcinoma 2	11.0
Colon cancer NAT 3	17.6	Prostate adenocarcinoma 3	36.6
Colon malignant cancer 4	52.9	Prostate adenocarcinoma 4	38.4
Colon normal adjacent tissue 4	20.6	Prostate cancer NAT 5	12.4
Lung cancer 1	20.3	Prostate adenocarcinoma 6	16.4

Lung NAT 1	5.1	Prostate adenocarcinoma 7	20.6
Lung cancer 2	88.9	Prostate adenocarcinoma 8	13.6
Lung NAT 2	9.5	Prostate adenocarcinoma 9	62.9
Squamous cell carcinoma 3	39.8	Prostate cancer NAT 10	10.9
Lung NAT 3	4.4	Kidney cancer 1	39.5
metastatic melanoma 1	31.6	KidneyNAT 1	23.8
Melanoma 2	5.6	Kidney cancer 2	100.0
Melanoma 3	4.8	Kidney NAT 2	31.6
metastatic melanoma 4	46.7	Kidney cancer 3	33.9
metastatic melanoma 5	84.7	Kidney NAT 3	8.5
Bladder cancer 1	3.4	Kidney cancer 4	13.5
Bladder cancer NAT 1	0.0	Kidney NAT 4	6.3
Bladder cancer 2	23.7		

CNS_neurodegeneration_v1.0 Summary: Ag3649 This panel does not show differential expression of this gene in Alzheimer's disease. However, this profile confirms the expression of this gene at moderate levels in the brain. See Panel 1.4 for discussion of this gene in the central nervous system.

5   **General_screening_panel_v1.4 Summary:** Ag3649 Highest expression of this gene is seen in a brain cancer cell line (CT=25). This gene is widely expressed in this panel, with high levels of expression seen in brain, colon, gastric, lung, breast, ovarian, and melanoma cancer cell lines. This expression profile suggests a role for this gene product in cell survival and proliferation. Modulation of this gene product may be useful in the

10   treatment of cancer.

Among tissues with metabolic function, this gene is expressed at high to moderate levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic function and that

15   disregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

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In addition, this gene is expressed at much higher levels in fetal lung tissue (CT=26) when compared to expression in the adult counterpart (CT=29). Thus, expression of this gene may be used to differentiate between the fetal and adult source of this tissue.

This gene is also expressed at high to moderate levels in the CNS, including the
5   hippocampus, thalamus, substantia nigra, amygdala, cerebellum and cerebral cortex. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Panel 4.1D Summary: Ag3649 Highest expression of this gene is seen in IL-9
10   treated NCI-H292 cells and TNF-a and IL-1b treated keratinocytes (CT=27.3). This gene is also expressed at hight to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues
15   represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.4 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic
20   may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

general oncology screening panel_v_2.4 Summary: Ag3649 Highest expression
25   of this gene is detected in kidney cancer (CT=27.6). Significant expression of this gene is detected both in normal and cancer samples derived from colon, kidney, bladder, lung, prostate and melanoma. Expression of this gene is higher in cancer samples as compared to the corresponding normal adjacent samples. Therefore, expression of this gene may be use as diagnostic marker for lung, colon, prostate, kidney and bladder cancer, as well as
30   metastatic melanoma. In addition, therapeutic modulation of this gene through the use of antibodoy or small molecule drug may be beneficial in the treatment of melenoma, prostate, lung, colon, kidney and bladder cancers.

BB. CG97012-01 and CG97012-02: SEIZURE 6 PRECURSOR PROTEIN-LIKE PROTEIN.

Expression of gene CG97012-01 and CG97012-02 was assessed using the primer-probe sets Ag1477 and Ag4105, described in Tables BBA and BBB. Results of the RTQ-PCR runs are shown in Tables BBC, BBD, BBE, BBF, BBG, BBH, BBI and BBJ.

Table BBA. Probe Name Ag1477

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aatcctgaggggtacattgact-3'	22	859	771
Probe	TET-5'-ccctcaacaactttctggagtgcaca-3'-TAMRA	26	902	772
Reverse	5'-agccagtgtagactgtcacgtt-3'	22	931	773

Table BBB. Probe Name Ag4105

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aatcctgaggggtacattgact-3'	22	859	774
Probe	TET-5'-ccctcaacaactttctggagtgcaca-3'-TAMRA	26	902	775
Reverse	5'-agccagtgtagactgtcacgtt-3'	22	931	776

Table BBC. A1_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag4105, Run 255325336	Tissue Name	Rel. Exp.(%) Ag4105, Run 255325336
110967 COPD-F	7.7	112427 Match Control Psoriasis-F	1.3
110980 COPD-F	1.9	112418 Psoriasis-M	1.1
110968 COPD-M	0.0	112723 Match Control Psoriasis-M	3.9
110977 COPD-M	4.4	112419 Psoriasis-M	0.0

110989 Emphysema-F	9.6	112424 Match Control Psoriasis-M	1.2
110992 Emphysema-F	1.6	112420 Psoriasis-M	8.2
110993 Emphysema-F	13.8	112425 Match Control Psoriasis-M	5.8
110994 Emphysema-F	0.0	104689 (MF) OA Bone-Backus	6.7
110995 Emphysema-F	0.0	104690 (MF) Adj "Normal" Bone-Backus	1.9
110996 Emphysema-F	0.0	104691 (MF) OA Synovium-Backus	49.3
110997 Asthma-M	4.5	104692 (BA) OA Cartilage-Backus	36.6
111001 Asthma-F	0.0	104694 (BA) OA Bone-Backus	7.9
111002 Asthma-F	1.8	104695 (BA) Adj "Normal" Bone-Backus	3.7
111003 Atopic Asthma-F	5.8	104696 (BA) OA Synovium-Backus	22.1
111004 Atopic Asthma-F	6.9	104700 (SS) OA Bone-Backus	4.2
111005 Atopic Asthma-F	3.1	104701 (SS) Adj "Normal" Bone-Backus	6.6
111006 Atopic Asthma-F	0.0	104702 (SS) OA Synovium-Backus	15.1
111417 Allergy-M	0.0	117093 OA Cartilage Rep7	5.8
112347 Allergy-M	15.2	112672 OA Bone5	3.7
112349 Normal Lung-F	11.0	112673 OA Synovium5	0.0
112357 Normal Lung-F	2.2	112674 OA Synovial Fluid cells5	1.7
112354 Normal Lung-M	7.1	117100 OA Cartilage Rep14	0.0
112374 Crohns-F	25.0	112756 OA Bone9	100.0
112389 Match Control Crohns-F	0.9	112757 OA Synovium9	6.0
112375 Crohns-F	8.3	112758 OA Synovial Fluid Cells9	6.3

112732 Match Control Crohns-F	3.3	117125 RA Cartilage Rep2	1.8
112725 Crohns-M	7.4	113492 Bone2 RA	14.8
112387 Match Control Crohns-M	2.7	113493 Synovium2 RA	3.0
112378 Crohns-M	20.9	113494 Syn Fluid Cells RA	11.6
112390 Match Control Crohns-M	6.9	113499 Cartilage4 RA	10.7
112726 Crohns-M	15.3	113500 Bone4 RA	7.1
112731 Match Control Crohns-M	5.9	113501 Synovium4 RA	5.4
112380 Ulcer Col-F	2.1	113502 Syn Fluid Cells4 RA	2.0
112734 Match Control Ulcer Col-F	2.0	113495 Cartilage3 RA	2.0
112384 Ulcer Col-F	2.1	113496 Bone3 RA	14.5
112737 Match Control Ulcer Col-F	1.4	113497 Synovium3 RA	6.8
112386 Ulcer Col-F	4.2	113498 Syn Fluid Cells3 RA	10.5
112738 Match Control Ulcer Col-F	1.9	117106 Normal Cartilage Rep20	0.0
112381 Ulcer Col-M	5.8	113663 Bone3 Normal	8.3
112735 Match Control Ulcer Col-M	39.0	113664 Synovium3 Normal	8.8
112382 Ulcer Col-M	11.1	113665 Syn Fluid Cells3 Normal	8.2
112394 Match Control Ulcer Col-M	2.0	117107 Normal Cartilage Rep22	2.3
112383 Ulcer Col-M	4.9	113667 Bone4 Normal	9.4
112736 Match Control Ulcer Col-M	0.0	113668 Synovium4 Normal	4.7
112423 Psoriasis-F	5.5	113669 Syn Fluid Cells4 Normal	0.0

Table BBD. Ardais Panel v.1.0

Tissue Name	Rel. Exp.(%) Ag1477, Run 263245998	Tissue Name	Rel. Exp.(%) Ag1477, Run 263245998
136799_Lung cancer(362)	5.4	136787_lung cancer(356)	2.4
136800_Lung NAT(363)	49.3	136788_lung NAT(357)	17.8
136813_Lung cancer(372)	5.4	136804_Lung cancer(369)	9.9
136814_Lung NAT(373)	6.2	136805_Lung NAT(36A)	12.8
136815_Lung cancer(374)	18.0	136806_Lung cancer(36B)	1.7
136816_Lung NAT(375)	62.4	136807_Lung NAT(36C)	19.6
136791_Lung cancer(35A)	3.8	136789_lung cancer(358)	15.0
136795_Lung cancer(35E)	1.9	136802_Lung cancer(365)	21.2
136797_Lung cancer(360)	0.0	136803_Lung cancer(368)	7.7
136794_lung NAT(35D)	24.5	136811_Lung cancer(370)	5.1
136818_Lung NAT(377)	33.2	136810_Lung NAT(36F)	100.0

Table BBE. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag1477, Run 206941434	Rel. Exp.(%) Ag4105, Run 206943848	Tissue Name	Rel. Exp.(%) Ag1477, Run 206941434	Rel. Exp.(%) Ag4105, Run 206943848
AD 1 Hippo	11.9	10.6	Control (Path) 3 Temporal Ctx	2.6	2.6
AD 2 Hippo	33.7	23.3	Control (Path) 4 Temporal Ctx	29.3	17.9
AD 3 Hippo	8.1	7.0	AD 1 Occipital Ctx	7.9	7.7
AD 4 Hippo	5.1	5.0	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	100.0	100.0	AD 3 Occipital Ctx	3.9	3.2
AD 6 Hippo	49.7	40.9	AD 4 Occipital Ctx	17.2	10.5
Control 2 Hippo	61.1	47.0	AD 5 Occipital Ctx	15.1	55.5
Control 4 Hippo	4.1	3.8	AD 6 Occipital Ctx	69.3	14.1

Control (Path) 3 Hippo	3.7	3.3	Control 1 Occipital Ctx	1.2	0.8
AD 1 Temporal Ctx	6.1	4.7	Control 2 Occipital Ctx	88.3	84.7
AD 2 Temporal Ctx	27.0	23.8	Control 3 Occipital Ctx	16.2	13.4
AD 3 Temporal Ctx	3.1	2.6	Control 4 Occipital Ctx	2.3	2.3
AD 4 Temporal Ctx	14.4	10.3	Control (Path) 1 Occipital Ctx	92.7	73.7
AD 5 Inf Temporal Ctx	66.9	71.2	Control (Path) 2 Occipital Ctx	5.4	7.0
AD 5 SupTemporal Ctx	36.1	32.3	Control (Path) 3 Occipital Ctx	1.1	0.4
AD 6 Inf Temporal Ctx	25.7	25.3	Control (Path) 4 Occipital Ctx	14.1	10.6
AD 6 Sup Temporal Ctx	27.4	22.5	Control 1 Parietal Ctx	3.9	2.2
Control 1 Temporal Ctx	4.5	3.9	Control 2 Parietal Ctx	15.8	19.2
Control 2 Temporal Ctx	52.9	42.0	Control 3 Parietal Ctx	17.4	14.9
Control 3 Temporal Ctx	14.8	11.4	Control (Path) 1 Parietal Ctx	99.3	92.7
Control 4 Temporal Ctx	4.9	4.4	Control (Path) 2 Parietal Ctx	23.7	16.0
Control (Path) 1 Temporal Ctx	69.3	57.8	Control (Path) 3 Parietal Ctx	2.1	2.7
Control (Path) 2 Temporal Ctx	33.0	23.7	Control (Path) 4 Parietal Ctx	58.2	29.5

Table BBF. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag1477, Run 213323518	Rel. Exp.(%) Ag4105, Run 212714156	Tissue Name	Rel. Exp.(%) Ag1477, Run 213323518	Rel. Exp.(%) Ag4105, Run 212714156
Adipose	0.2	0.1	Renal ca. TK-10	0.0	0.0

Melanoma* Hs688(A).T	0.0	0.0	Bladder	0.6	0.3
Melanoma* Hs688(B).T	0.0	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW-948	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	Colon ca. SW480	0.0	0.0
Squamous cell carcinoma SCC-4	0.0	0.0	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	0.2	0.1	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.0	Colon ca. HCT-116	0.0	0.0
Prostate Pool	0.2	0.1	Colon ca. CaCo-2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	0.0	0.0
Uterus Pool	0.0	0.0	Colon ca. SW1116	0.0	0.0
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo-205	0.0	0.0
Ovarian ca. SK-OV-3	6.5	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.0	0.0	Colon Pool	0.1	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.4	0.2
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	6.0	0.1
Ovarian ca. OVCAR-8	0.0	0.0	Bone Marrow Pool	0.1	0.1
Ovary	0.1	0.1	Fetal Heart	0.1	0.0
Breast ca. MCF-7	0.0	0.0	Heart Pool	0.1	0.0
Breast ca. MDA-MB-231	0.0	0.0	Lymph Node Pool	0.3	0.1
Breast ca. BT 549	0.0	0.0	Fetal Skeletal Muscle	0.2	0.0
Breast ca. T47D	0.0	0.1	Skeletal Muscle Pool	0.0	0.0

Breast ca. MDA-N	0.0	0.0	Spleen Pool	0.1	0.1
Breast Pool	0.0	0.1	Thymus Pool	0.2	0.2
Trachea	0.2	0.3	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	1.2	1.0
Fetal Lung	0.6	0.3	CNS cancer (neuro;met) SK-N-AS	0.0	0.0
Lung ca. NCI-N417	30.1	11.4	CNS cancer (astro) SF-539	0.0	0.0
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.3	0.1
Lung ca. NCI-H146	22.2	18.3	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	9.0	4.3	CNS cancer (glio) SF-295	0.0	0.0
Lung ca. A549	0.0	0.0	Brain (Amygdala) Pool	21.8	9.3
Lung ca. NCI-H526	11.0	4.3	Brain (cerebellum)	87.1	54.3
Lung ca. NCI-H23	1.3	0.7	Brain (fetal)	**100.0**	**100.0**
Lung ca. NCI-H460	0.2	0.1	Brain (Hippocampus) Pool	28.9	25.5
Lung ca. HOP-62	0.0	0.0	Cerebral Cortex Pool	40.9	15.9
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	29.3	12.1
Liver	0.0	0.0	Brain (Thalamus) Pool	37.9	14.7
Fetal Liver	0.1	0.2	Brain (whole)	43.5	26.4
Liver ca. HepG2	0.0	0.0	Spinal Cord Pool	7.5	4.0
Kidney Pool	0.1	0.0	Adrenal Gland	4.3	1.5
Fetal Kidney	0.1	0.0	Pituitary gland Pool	2.9	2.9
Renal ca. 786-0	0.0	0.0	Salivary Gland	0.2	0.1

Renal ca. A498	0.0	0.0	Thyroid (female)	0.1	0.2
Renal ca. ACHN	0.0	0.0	Pancreatic ca. CAPAN2	0.0	0.0
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.6	0.2

Table BBG. Panel 3D

Tissue Name	Rel. Exp.(%) Ag1477, Run 215538905	Tissue Name	Rel. Exp.(%) Ag1477, Run 215538905
Daoy- Medulloblastoma	0.0	Ca Ski- Cervical epidermoid carcinoma (metastasis)	0.0
TE671- Medulloblastoma	0.0	ES-2- Ovarian clear cell carcinoma	0.0
D283 Med- Medulloblastoma	0.0	Ramos- Stimulated with PMA/ionomycin 6h	0.0
PFSK-1- Primitive Neuroectodermal	0.0	Ramos- Stimulated with PMA/ionomycin 14h	0.0
XF-498- CNS	0.7	MEG-01- Chronic myelogenous leukemia (megokaryoblast)	0.0
SNB-78- Glioma	0.0	Raji- Burkitt's lymphoma	0.0
SF-268- Glioblastoma	0.0	Daudi- Burkitt's lymphoma	0.0
T98G- Glioblastoma	0.0	U266- B-cell plasmacytoma	0.0
SK-N-SH- Neuroblastoma (metastasis)	3.8	CA46- Burkitt's lymphoma	0.0
SF-295- Glioblastoma	0.0	RL- non-Hodgkin's B-cell lymphoma	0.0
Cerebellum	34.6	JM1- pre-B-cell lymphoma	0.0
Cerebellum	50.7	Jurkat- T cell leukemia	0.0
NCI-H292- Mucoepidermoid lung carcinoma	0.3	TF-1- Erythroleukemia	0.0
DMS-114- Small cell lung cancer	0.6	HUT 78- T-cell lymphoma	0.0
DMS-79- Small cell lung cancer	100.0	U937- Histiocytic lymphoma	0.0
NCI-H146- Small cell lung cancer	61.1	KU-812- Myelogenous leukemia	0.0

NCI-H526- Small cell lung cancer	49.0	769-P- Clear cell renal carcinoma	0.0
NCI-N417- Small cell lung cancer	78.5	Caki-2- Clear cell renal carcinoma	0.0
NCI-H82- Small cell lung cancer	23.7	SW 839- Clear cell renal carcinoma	0.0
NCI-H157- Squamous cell lung cancer (metastasis)	0.0	G401- Wilms' tumor	0.0
NCI-H1155- Large cell lung cancer	18.8	Hs766T- Pancreatic carcinoma (LN metastasis)	0.0
NCI-H1299- Large cell lung cancer	0.0	CAPAN-1- Pancreatic adenocarcinoma (liver metastasis)	0.0
NCI-H727- Lung carcinoid	1.7	SU86.86- Pancreatic carcinoma (liver metastasis)	0.0
NCI-UMC-11- Lung carcinoid	0.0	BxPC-3- Pancreatic adenocarcinoma	0.0
LX-1- Small cell lung cancer	0.0	HPAC- Pancreatic adenocarcinoma	0.0
Colo-205- Colon cancer	0.0	MIA PaCa-2- Pancreatic carcinoma	0.0
KM12- Colon cancer	0.1	CFPAC-1- Pancreatic ductal adenocarcinoma	0.0
KM20L2- Colon cancer	0.0	PANC-1- Pancreatic epithelioid ductal carcinoma	0.0
NCI-H716- Colon cancer	0.0	T24- Bladder carcinma (transitional cell)	0.0
SW-48- Colon adenocarcinoma	0.0	5637- Bladder carcinoma	0.0
SW1116- Colon adenocarcinoma	0.0	HT-1197- Bladder carcinoma	0.0
LS 174T- Colon adenocarcinoma	0.0	UM-UC-3- Bladder carcinma (transitional cell)	0.0
SW-948- Colon adenocarcinoma	0.0	A204- Rhabdomyosarcoma	0.0
SW-480- Colon adenocarcinoma	0.0	HT-1080- Fibrosarcoma	0.0
NCI-SNU-5- Gastric carcinoma	0.0	MG-63- Osteosarcoma	0.0

KATO III- Gastric carcinoma	0.0	SK-LMS-1- Leiomyosarcoma (vulva)	0.0
NCI-SNU-16- Gastric carcinoma	0.0	SJRH30- Rhabdomyosarcoma (met to bone marrow)	0.0
NCI-SNU-1- Gastric carcinoma	0.0	A431- Epidermoid carcinoma	0.0
RF-1- Gastric adenocarcinoma	0.2	WM266-4- Melanoma	0.0
RF-48- Gastric adenocarcinoma	0.0	DU 145- Prostate carcinoma (brain metastasis)	0.0
MKN-45- Gastric carcinoma	2.7	MDA-MB-468- Breast adenocarcinoma	0.0
NCI-N87- Gastric carcinoma	0.0	SCC-4- Squamous cell carcinoma of tongue	0.0
OVCAR-5- Ovarian carcinoma	0.0	SCC-9- Squamous cell carcinoma of tongue	0.0
RL95-2- Uterine carcinoma	0.0	SCC-15- Squamous cell carcinoma of tongue	0.0
HelaS3- Cervical adenocarcinoma	0.0	CAL 27- Squamous cell carcinoma of tongue	0.0

Table BBH. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag1477, Run 200923970	Rel. Exp.(%) Ag4105, Run 175180105	Tissue Name	Rel. Exp.(%) Ag1477, Run 200923970	Rel. Exp.(%) Ag4105, Run 175180105
Secondary Th1 act	0.0	0.0	HUVEC IL-1beta	0.0	0.0
Secondary Th2 act	0.0	0.0	HUVEC IFN gamma	0.0	0.0
Secondary Tr1 act	4.5	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	3.3	0.0	HUVEC IL-11	0.0	0.9
Secondary Tr1 rest	0.0	0.0	Lung Microvascular EC none	0.0	7.0
Primary Th1 act	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0

Primary Th2 act	0.0	0.0	Microvascular Dermal EC none	0.0	0.0
Primary Tr1 act	1.5	0.0	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0
Primary Th2 rest	0.0	0.0	Small airway epithelium none	0.0	0.0
Primary Tr1 rest	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	0.0	4.0	Coronery artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	0.0	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	0.0	3.9	Astrocytes rest	4.1	0.0
Secondary CD8 lymphocyte rest	0.0	1.4	Astrocytes TNFalpha + IL-1beta	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	KU-812 (Basophil) rest	0.0	0.0
CD4 lymphocyte none	5.6	2.6	KU-812 (Basophil) PMA/ionomycin	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	2.6	1.4	CCD1106 (Keratinocytes) none	0.0	0.0
LAK cells rest	0.0	2.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	4.1	1.1	Liver cirrhosis	0.0	0.0
LAK cells IL-2+IL-12	0.0	0.0	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	NCI-H292 IL-4	0.0	0.0
LAK cells IL-2+ IL-18	0.0	0.0	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	0.0	0.0	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	11.7	0.0	NCI-H292 IFN gamma	0.0	0.0

Two Way MLR 3 day	4.7	0.0	HPAEC none	0.0	0.0
Two Way MLR 5 day	0.0	0.0	HPAEC TNF alpha + IL-1 beta	0.0	0.0
Two Way MLR 7 day	0.0	0.0	Lung fibroblast none	0.0	0.0
PBMC rest	26.8	8.5	Lung fibroblast TNF alpha + IL-1 beta	0.0	0.0
PBMC PWM	0.0	0.0	Lung fibroblast IL-4	0.0	0.0
PBMC PHA-L	0.0	0.0	Lung fibroblast IL-9	7.2	0.0
Ramos (B cell) none	0.0	0.0	Lung fibroblast IL-13	0.0	2.2
Ramos (B cell) ionomycin	0.0	0.0	Lung fibroblast IFN gamma	0.0	0.0
B lymphocytes PWM	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	0.6
B lymphocytes CD40L and IL-4	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0	0.0
EOL-1 dbcAMP	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	0.0	Dermal fibroblast IFN gamma	3.5	0.0
Dendritic cells none	35.1	11.5	Dermal fibroblast IL-4	0.0	0.0
Dendritic cells LPS	9.4	2.3	Dermal Fibroblasts rest	1.6	0.0
Dendritic cells anti-CD40	24.5	14.1	Neutrophils TNFa+LPS	7.5	0.0
Monocytes rest	93.3	37.6	Neutrophils rest	3.8	3.1
Monocytes LPS	5.6	2.5	Colon	17.6	5.8
Macrophages rest	0.0	0.0	Lung	1.2	4.5
Macrophages LPS	1.7	0.0	Thymus	49.3	13.8
HUVEC none	0.0	0.0	Kidney	100.0	100.0
HUVEC starved	0.0	0.0			

Table BB1. Panel CNS_1.1

Tissue Name	Rel. Exp.(%) Ag1477, Run 204172546	Tissue Name	Rel. Exp.(%) Ag1477, Run 204172546

Cing Gyr Depression2	4.2	BA17 PSP2	3.6
Cing Gyr Depression	2.3	BA17 PSP	11.1
Cing Gyr PSP2	1.3	BA17 Huntington's2	3.4
Cing Gyr PSP	2.9	BA17 Huntington's	13.7
Cing Gyr Huntington's2	4.4	BA17 Parkinson's2	13.5
Cing Gyr Huntington's	27.5	BA17 Parkinson's	7.7
Cing Gyr Parkinson's2	10.4	BA17 Alzheimer's2	1.7
Cing Gyr Parkinson's	9.8	BA17 Control2	21.5
Cing Gyr Alzheimer's2	3.4	BA17 Control	16.6
Cing Gyr Alzheimer's	9.6	BA9 Depression2	3.0
Cing Gyr Control2	19.8	BA9 Depression	2.2
Cing Gyr Control	24.1	BA9 PSP2	2.6
Temp Pole Depression2	2.4	BA9 PSP	5.1
Temp Pole PSP2	2.9	BA9 Huntington's2	2.0
Temp Pole PSP	0.9	BA9 Huntington's	16.0
Temp Pole Huntington's	13.6	BA9 Parkinson's2	33.2
Temp Pole Parkinson's2	9.4	BA9 Parkinson's	10.2
Temp Pole Parkinson's	7.2	BA9 Alzheimer's2	3.6
Temp Pole Alzheimer's2	1.3	BA9 Alzheimer's	1.1
Temp Pole Alzheimer's	2.2	BA9 Control2	**100.0**
Temp Pole Control2	15.8	BA9 Control	8.7
Temp Pole Control	6.2	BA7 Depression	3.6
Glob Palladus Depression	0.8	BA7 PSP2	7.8
Glob Palladus PSP2	1.5	BA7 PSP	19.3
Glob Palladus PSP	0.5	BA7 Huntington's2	7.6
Glob Palladus Parkinson's2	0.8	BA7 Huntington's	13.1

Glob Palladus Parkinson's	13.4	BA7 Parkinson's2	16.8
Glob Palladus Alzheimer's2	1.3	BA7 Parkinson's	2.7
Glob Palladus Alzheimer's	3.1	BA7 Alzheimer's2	1.3
Glob Palladus Control2	1.9	BA7 Control2	14.4
Glob Palladus Control	1.0	BA7 Control	14.5
Sub Nigra Depression2	1.5	BA4 Depression2	3.1
Sub Nigra Depression	0.8	BA4 Depression	6.8
Sub Nigra PSP2	1.2	BA4 PSP2	15.1
Sub Nigra Huntington's2	10.6	BA4 PSP	4.6
Sub Nigra Huntington's	15.1	BA4 Huntington's2	0.9
Sub Nigra Parkinson's2	12.5	BA4 Huntington's	21.6
Sub Nigra Alzheimer's2	2.0	BA4 Parkinson's2	40.3
Sub Nigra Control2	9.0	BA4 Parkinson's	17.1
Sub Nigra Control	8.4	BA4 Alzheimer's2	2.0
BA17 Depression2	6.7	BA4 Control2	26.4
BA17 Depression	2.0	BA4 Control	12.5

Table BBJ. general oncology screening panel_v_2.4

Tissue Name	Rel. Exp.(%) Ag1477, Run 259733191	Tissue Name	Rel. Exp.(%) Ag1477, Run 259733191
Colon cancer 1	2.8	Bladder NAT 2	0.0
Colon NAT 1	12.6	Bladder NAT 3	0.0
Colon cancer 2	10.9	Bladder NAT 4	1.4
Colon NAT 2	0.0	Prostate adenocarcinoma 1	100.0
Colon cancer 3	0.0	Prostate adenocarcinoma 2	4.9
Colon NAT 3	30.6	Prostate adenocarcinoma 3	17.7

Colon malignant cancer 4	0.0	Prostate adenocarcinoma 4	0.0
Colon NAT 4	1.3	Prostate NAT 5	8.2
Lung cancer 1	5.8	Prostate adenocarcinoma 6	7.0
Lung NAT 1	0.0	Prostate adenocarcinoma 7	2.8
Lung cancer 2	42.0	Prostate adenocarcinoma 8	5.6
Lung NAT 2	0.0	Prostate adenocarcinoma 9	48.6
Squamous cell carcinoma 3	0.0	Prostate NAT 10	0.0
Lung NAT 3	0.0	Kidney cancer 1	0.0
Metastatic melanoma 1	5.3	Kidney NAT 1	6.1
Melanoma 2	2.1	Kidney cancer 2	9.7
Melanoma 3	0.9	Kidney NAT 2	0.0
Metastatic melanoma 4	11.8	Kidney cancer 3	1.8
Metastatic melanoma 5	17.7	Kidney NAT 3	0.0
Bladder cancer 1	1.3	Kidney cancer 4	0.0
Bladder NAT 1	0.0	Kidney NAT 4	0.0
Bladder cancer 2	0.0		

AI_comprehensive panel_v1.0 Summary: Ag4105 Highest expression in an sample from OA bone (CT=31.4). Low to moderate levels of expression of this gene are detected in samples derived from osteoarthritic (OA) bone and adjacent bone as well as OA cartilage and OA synovium. Low level expression is also detected in cartilage, bone, and

5 synovial fluid samples from rheumatoid arthritis patients. Low level expression is also detected in samples derived from normal lung samples, COPD lung, emphysema, allergy, Crohn's disease (normal matched control and diseased), and ulcerative colitis (normal matched control and diseased). Therefore, therapeutic modulation of this gene product may ameliorate symptoms/conditions associated with autoimmune and inflammatory disorders

10 including psoriasis, allergy, asthma, inflammatory bowel disease, rheumatoid arthritis and osteoarthritis.

Ardais Panel v.1.0 Summary: Ag1477 Highest expression of this gene is seen in normal lung tissue adjacent to a tumor (CT=31.6). In addition, this gene is expressed at low but significant levels in both lung tumor and normal tissue. The expression in normal adjacent tissue is however, higher compared to the tumor tissue. Therefore, therapeutic

5   modulation of this gene or its protein product may be useful in the treatment of lung cancer

CNS_neurodegeneration_v1.0 Summary: Ag1477/Ag4105 Two experiments with the same probe and primer set produce results that are in excellent agreement. This panel confirms expression of this gene at high levels in the brain, with highest expression detected in the hippocampus of an Alzheimer's patient (CTs=25-26). In addition, this gene

10   appears to be slightly down-regulated in the temporal cortex of Alzheimer's disease patients. Therefore, up-regulation of this gene or its protein product, or treatment with specific agonists for this receptor may be of use in reversing the dementia, memory loss, and neuronal death associated with this disease.

General_screening_panel_v1.4 Summary: Ag1477/Ag4105 Two experiments

15   with the same probe and primer set produce results that are in excellent agreement. Highest expression of this gene is detected in the fetal brain (CT=25-26). In addition, high to moderate levels of expression of this gene are seen in all regions of the CNS examined, including the hippocampus, thalamus, substantia nigra, amygdala, cerebellum and cerebral cortex. Therefore, therapeutic modulation of the expression or function of this gene may be

20   useful in the treatment of neurological disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

In addition, this gene is expressed in a cluster of cell line samples derived from lung cancer. This gene is homologous to seizure-related gene 6, a gene clearly involved in lung tumorogenesis. The genetic data from Nishioka *et al.* point to its genomic region as being

25   involved in lung tumors. While the region itself is often deleted, the expression indicates that the deleted regions might be regulatory region(s) that normally repress the expression of this gene in lung tumor cells. Therefore, targeting this gene with a human monoclonal antibody that results in an inhibition of the activity of this protein, preferably as it relates to its apoptotic/survival activity in tumor cells, specifically lung tumor cells, may have a

30   therapeutic effect on all solid tumor that depend on its activity, preferably on lung tumors.

References:

1. Nishioka M. Oncogene 2000 Dec 14;19(54):6251-60

2. Shimizu-Nishikawa K. Biochem Biophys Res Commun 1995 Nov 2;216(1):382-9

Panel 3D Summary: Ag1477 Expression in this panel is consistent with expression in Panel 1.4, with expression detected in samples derived from cerebellum and lung cancer
5 cell lines only.

Panel 4.1D Summary: Ag1477/Ag4105 Two experiments with the same probe and primer set produce results that are in excellent agreement. Highest expression is seen in the kidney, with moderate to low levels of expression seen in resting monocytes, and dendritic cells. The transcript is more highly expressed in resting monocytes and dendritic cells than
10 in treated cells of these types. Thus, the protein encoded by this transcript may be important in monocytic and dendritic cell differentiation and activation. Therefore, regulating the expression of this transcript or the function of the protein it encodes may alter the types and levels of monocytic cells regulated by cytokine and chemokine production and T cell activation. Therapeutics designed with the protein encoded by this transcript could therefore
15 be important for the treatment of asthma, emphysema, inflammatory bowel disease, arthritis and psoriasis.

Panel 5D Summary: Ag1477 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

Panel CNS_1.1 Summary: Ag1477 This panel confirms the expression of this
20 gene at moderate levels in the brain. See Panels 1.4 and CNS_neurodegeneration_v1.0 for discussion of this gene in the central nervous system.

general oncology screening panel_v_2.4 Summary: Ag1477 Highest expression of this gene is seen in prostate cancer (CT=33). Low but significant levels of expression are also seen in a lung cancer and normal colon. Hence the product of this gene can be used as a
25 marker and therapeutic modulation may lead to treatment of cancer.

BC. CG97012-03: SEIZURE 6 PRECURSOR PROTEIN-LIKE PROTEIN.

Expression of gene CG97012-03 was assessed using the primer-probe set Ag6660, described in Table BCA. Results of the RTQ-PCR runs are shown in Tables BCB and BCC.

30   Table BCA. Probe Name Ag6660

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-tatgacatcgtggggagtga-3'	20	1159	777
Probe	TET-5'-ctcacctgccagtgggacctcag-3'-TAMRA	23	1183	778
Reverse	5'-gactcctccgttttctcacaa-3'	21	1227	779

Table BCB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag6660, Run 276247136	Tissue Name	Rel. Exp.(%) Ag6660, Run 276247136
AD 1 Hippo	14.8	Control (Path) 3 Temporal Ctx	2.0
AD 2 Hippo	31.0	Control (Path) 4 Temporal Ctx	26.4
AD 3 Hippo	0.0	AD 1 Occipital Ctx	3.3
AD 4 Hippo	8.2	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	63.3	AD 3 Occipital Ctx	2.9
AD 6 Hippo	66.0	AD 4 Occipital Ctx	11.7
Control 2 Hippo	76.3	AD 5 Occipital Ctx	47.6
Control 4 Hippo	3.9	AD 6 Occipital Ctx	11.9
Control (Path) 3 Hippo	2.2	Control 1 Occipital Ctx	0.8
AD 1 Temporal Ctx	2.7	Control 2 Occipital Ctx	71.2
AD 2 Temporal Ctx	20.0	Control 3 Occipital Ctx	8.7
AD 3 Temporal Ctx	2.7	Control 4 Occipital Ctx	0.0
AD 4 Temporal Ctx	11.8	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	83.5	Control (Path) 2 Occipital Ctx	9.3
AD 5 Sup Temporal Ctx	53.6	Control (Path) 3 Occipital Ctx	1.4
AD 6 Inf Temporal Ctx	29.5	Control (Path) 4 Occipital Ctx	10.9
AD 6 Sup Temporal Ctx	31.0	Control 1 Parietal Ctx	1.8

Control 1 Temporal Ctx	0.4	Control 2 Parietal Ctx	22.8
Control 2 Temporal Ctx	47.3	Control 3 Parietal Ctx	13.9
Control 3 Temporal Ctx	8.2	Control (Path) 1 Parietal Ctx	87.1
Control 3 Temporal Ctx	4.4	Control (Path) 2 Parietal Ctx	17.3
Control (Path) 1 Temporal Ctx	80.1	Control (Path) 3 Parietal Ctx	1.4
Control (Path) 2 Temporal Ctx	32.8	Control (Path) 4 Parietal Ctx	48.3

Table BCC. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6660, Run 277258095	Tissue Name	Rel. Exp.(%) Ag6660, Run 277258095
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.1
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0

Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.2
Breast Pool	0.0	Thymus Pool	0.1
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	1.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	12.2	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	18.7	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.7	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	31.6
Lung ca. NCI-H526	4.9	Brain (cerebellum)	99.3
Lung ca. NCI-H23	0.0	Brain (fetal)	**100.0**
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	39.2
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	53.6
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	21.0
Liver	0.0	Brain (Thalamus) Pool	73.2
Fetal Liver	0.0	Brain (whole)	67.4
Liver ca. HepG2	0.0	Spinal Cord Pool	3.6
Kidney Pool	0.0	Adrenal Gland	1.0
Fetal Kidney	0.0	Pituitary gland Pool	1.6

Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.2	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

CNS_neurodcgeneration_v1.0 Summary: Ag6660 This panel confirms the
expression of this gene at low levels in the brains of an independent group of individuals.
However, no differential expression of this gene was detected between Alzheimer's diseased
postmortem brains and those of non-demented controls in this experiment. See Panel 1.6 for

5   a discussion of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.6 Summary: Ag6660 Highest expression of this
gene is detected in fetal brain and cerebellum (CTs=28.8). In addition, moderate levels of
expression of this gene is mainly seen in all the regions of central nervous system including
amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal

10   cord. This gene codes for a variant of Seizure related gene 6 like (SEZ-6/SEZ6L). The
expression pattern of this gene is similar to the the one reported in mouse (Shimizu-
Nishikawa *et al.*, 1995, Brain Res Mol Brain Res 28:201-10, PMID: 7723619 ; Biochem
Biophys Res Commun 216(1):382-9, PMID: 7488116). Therefore, therapeutic modulation
of this gene product may be useful in the treatment of central nervous system disorders such

15   as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and
depression.

Moderate levels of expression of this gene is also seen in three of the lung cancer
cell lines. Furthermore, genetic and/or epigenetic SEZ6L alterations are involved in the
development and/or progression in a subset of lung cancer (Nishioka *et al.*, 2000, Oncogene

20   19(54):6251-60, PMID: 11175339). Therefore, therapeutic modulation of this gene product
through the use of antibodies or small molecule targe may be useful in the treatment of lung
cancer.

Panel 4.1D Summary: Ag6660 Expression of this gene is low/undetectable (CTs >
35) across all of the samples on this panel (data not shown).

25   **BD. CG99754-01: RIKEN-like protein**

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Expression of gene CG99754-01 was assessed using the primer-probe sets Gpcr07
and Ag07Gpcr, described in Tables BDA and BDB. Results of the RTQ-PCR runs are
shown in Tables BDC, BDD, BDE, BDF and BDG.

Table BDA. Probe Name Gpcr07

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctggaggttggcgacaatg-3'	19	511	780
Probe	TET-5'-cctcgtctacatctctcaccgcgcc-3'-TAMRA	25	531	781
Reverse	5'-ctgctccaggctgttgagg-3'	19	564	782

Table BDB. Probe Name Ag07Gpcr

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-ctggaggttggcgacaatg-3'	19	511	783
Probe	TET-5'-cctcgtctacatctctcaccgcgcc-3'-TAMRA	25	531	784
Reverse	5'-ctgctccaggctgttgagg-3'	19	564	785

Table BDC. CNS_neurodegeneration_v1.0.

Tissue Name	Rel. Exp.(%) Ag07Gpcr, Run 206989718	Rel. Exp.(%) Gpcr07, Run 224996509	Tissue Name	Rel. Exp.(%) Ag07Gpcr, Run 206989718	Rel. Exp.(%) Gpcr07, Run 224996509
AD 1 Hippo	26.2	8.5	Control (Path) 3 Temporal Ctx	2.0	5.6
AD 2 Hippo	64.2	30.4	Control (Path) 4 Temporal Ctx	42.9	41.2
AD 3 Hippo	3.5	9.4	AD 1 Occipital Ctx	14.3	15.6
AD 4 Hippo	11.3	8.2	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	59.9	78.5	AD 3 Occipital Ctx	3.6	5.0
AD 6 Hippo	81.2	40.9	AD 4 Occipital Ctx	23.8	18.8

Control 2 Hippo	53.2	39.5	AD 5 Occipital Ctx	28.5	16.8
Control 4 Hippo	11.2	6.0	AD 6 Occipital Ctx	57.0	57.0
Control (Path) 3 Hippo	3.3	4.5	Control 1 Occipital Ctx	0.0	4.6
AD 1 Temporal Ctx	17.2	11.7	Control 2 Occipital Ctx	46.0	68.8
AD 2 Temporal Ctx	34.2	30.1	Control 3 Occipital Ctx	21.5	18.8
AD 3 Temporal Ctx	1.7	7.7	Control 4 Occipital Ctx	3.4	6.2
AD 4 Temporal Ctx	28.3	18.7	Control (Path) 1 Occipital Ctx	94.0	100.0
AD 5 Inf Temporal Ctx	95.3	66.9	Control (Path) 2 Occipital Ctx	19.8	10.9
AD 5 SupTemporal Ctx	53.6	47.3	Control (Path) 3 Occipital Ctx	1.3	3.8
AD 6 Inf Temporal Ctx	55.9	36.6	Control (Path) 4 Occipital Ctx	28.9	19.1
AD 6 Sup Temporal Ctx	78.5	37.6	Control 1 Parietal Ctx	7.5	6.6
Control 1 Temporal Ctx	5.3	7.2	Control 2 Parietal Ctx	42.3	42.3
Control 2 Temporal Ctx	61.1	56.3	Control 3 Parietal Ctx	19.1	14.0
Control 3 Temporal Ctx	28.1	18.6	Control (Path) 1 Parietal Ctx	80.7	97.9
Control 4 Temporal Ctx	15.1	9.6	Control (Path) 2 Parietal Ctx	30.6	27.4
Control (Path) 1 Temporal Ctx	100.0	85.9	Control (Path) 3 Parietal Ctx	2.0	4.0
Control (Path) 2 Temporal Ctx	57.4	43.2	Control (Path) 4 Parietal Ctx	48.3	46.7

Table BDD. Panel 1

Tissue Name	Rel. Exp.(%) Gpcr07, Run 109664812	Tissue Name	Rel. Exp.(%) Gpcr07, Run 109664812

Endothelial cells	0.0	Renal ca. 786-0	0.0
Endothelial cells (treated)	0.0	Renal ca. A498	0.3
Pancreas	1.3	Renal ca. RXF 393	0.0
Pancreatic ca. CAPAN 2	0.0	Renal ca. ACHN	0.0
Adrenal gland	1.7	Renal ca. UO-31	0.0
Thyroid	1.3	Renal ca. TK-10	0.0
Salivary gland	3.0	Liver	2.1
Pituitary gland	2.5	Liver (fetal)	3.8
Brain (fetal)	52.5	Liver ca. (hepatoblast) HepG2	0.0
Brain (whole)	46.3	Lung	0.0
Brain (amygdala)	83.5	Lung (fetal)	0.7
Brain (cerebellum)	19.1	Lung ca. (small cell) LX-1	0.0
Brain (hippocampus)	100.0	Lung ca. (small cell) NCI-H69	3.7
Brain (substantia nigra)	43.5	Lung ca. (s.cell var.) SHP-77	0.2
Brain (thalamus)	59.5	Lung ca. (large cell)NCI-H460	2.1
Brain (hypothalamus)	0.7	Lung ca. (non-sm. cell) A549	4.2
Spinal cord	7.5	Lung ca. (non-s.cell) NCI-H23	6.8
glio/astro U87-MG	0.0	Lung ca. (non-s.cell) HOP-62	0.1
glio/astro U-118-MG	0.0	Lung ca. (non-s.cl) NCI-H522	3.8
astrocytoma SW1783	0.0	Lung ca. (squam.) SW 900	0.3
neuro*; met SK-N-AS	0.1	Lung ca. (squam.) NCI-H596	1.6
astrocytoma SF-539	0.8	Mammary gland	6.4
astrocytoma SNB-75	0.0	Breast ca.* (pl.ef) MCF-7	1.3
glioma SNB-19	1.5	Breast ca.* (pl.ef) MDA-MB-231	0.0
glioma U251	0.2	Breast ca.* (pl. ef) T47D	2.6

glioma SF-295	0.0	Breast ca. BT-549	0.0
Heart	5.3	Breast ca. MDA-N	1.3
Skeletal muscle	2.0	Ovary	5.6
Bone marrow	0.7	Ovarian ca. OVCAR-3	6.2
Thymus	0.5	Ovarian ca. OVCAR-4	0.3
Spleen	3.4	Ovarian ca. OVCAR-5	1.1
Lymph node	0.6	Ovarian ca. OVCAR-8	8.0
Colon (ascending)	1.6	Ovarian ca. IGROV-1	2.1
Stomach	1.3	Ovarian ca. (ascites) SK-OV-3	0.1
Small intestine	2.2	Uterus	2.2
Colon ca. SW480	0.5	Placenta	2.8
Colon ca.* SW620 (SW480 met)	0.1	Prostate	1.5
Colon ca. HT29	0.3	Prostate ca.* (bone met) PC-3	0.0
Colon ca. HCT-116	11.3	Testis	6.3
Colon ca. CaCo-2	0.7	Melanoma Hs688(A).T	0.0
Colon ca. HCT-15	0.0	Melanoma* (met) Hs688(B).T	0.1
Colon ca. HCC-2998	0.4	Melanoma UACC-62	9.8
Gastric ca. * (liver met) NCI-N87	0.4	Melanoma M14	3.3
Bladder	2.7	Melanoma LOX IMVI	0.0
Trachea	1.5	Melanoma* (met) SK-MEL-5	4.2
Kidney	2.9	Melanoma SK-MEL-28	2.9
Kidney (fetal)	51.8		

<u>Table BDE</u>. Panel 1.2

Tissue Name	Rel. Exp.(%) Gpcr07, Run 124273559	Rel. Exp.(%) Gpcr07, Run 126539429	Tissue Name	Rel. Exp.(%) Gpcr07, Run 124273559	Rel. Exp.(%) Gpcr07, Run 126539429
Endothelial cells	0.0	0.1	Renal ca. 786-0	0.0	0.0

Heart (Fetal)	2.8	2.8	Renal ca. A498	0.0	0.1
Pancreas	0.3	0.9	Renal ca. RXF 393	0.0	0.0
Pancreatic ca. CAPAN 2	0.0	0.0	Renal ca. ACHN	0.0	0.0
Adrenal Gland	1.7	1.5	Renal ca. UO-31	0.0	0.0
Thyroid	0.2	0.7	Renal ca. TK-10	0.0	0.0
Salivary gland	1.3	1.0	Liver	0.7	0.6
Pituitary gland	0.4	0.6	Liver (fetal)	1.3	1.0
Brain (fetal)	17.2	28.1	Liver ca. (hepatoblast) HepG2	0.0	0.0
Brain (whole)	34.9	39.2	Lung	0.1	0.1
Brain (amygdala)	40.6	29.7	Lung (fetal)	0.6	0.8
Brain (cerebellum)	5.3	9.9	Lung ca. (small cell) LX-1	0.0	0.1
Brain (hippocampus)	45.7	51.1	Lung ca. (small cell) NCI-H69	0.7	0.5
Brain (thalamus)	10.4	15.8	Lung ca. (s.cell var.) SHP-77	0.1	0.1
Cerebral Cortex	**100.0**	**100.0**	Lung ca. (large cell)NCI-H460	0.8	0.5
Spinal cord	3.8	3.1	Lung ca. (non-sm. cell) A549	2.0	1.0
glio/astro U87-MG	0.0	0.0	Lung ca. (non-s.cell) NCI-H23	1.7	0.9
glio/astro U-118-MG	0.0	0.0	Lung ca. (non-s.cell) HOP-62	0.0	0.0
astrocytoma SW1783	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	1.4	1.5
neuro*; met SK-N-AS	0.0	0.0	Lung ca. (squam.) SW 900	0.1	0.1
astrocytoma SF-539	0.2	0.2	Lung ca. (squam.) NCI-H596	0.4	0.5
astrocytoma SNB-75	0.0	0.0	Mammary gland	0.8	1.3
glioma SNB-19	0.4	0.3	Breast ca.* (pl.ef) MCF-7	0.2	0.2
glioma U251	0.0	0.1	Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0

glioma SF-295	0.0	0.0	Breast ca.* (pl. ef) T47D	0.3	0.6
Heart	2.8	1.6	Breast ca. BT-549	0.0	0.0
Skeletal Muscle	0.6	0.6	Breast ca. MDA-N	0.3	0.2
Bone marrow	0.1	0.1	Ovary	2.5	1.6
Thymus	0.1	0.1	Ovarian ca. OVCAR-3	0.9	1.1
Spleen	0.5	0.6	Ovarian ca. OVCAR-4	0.2	0.1
Lymph node	0.4	0.3	Ovarian ca. OVCAR-5	0.4	0.4
Colorectal Tissue	0.4	0.3	Ovarian ca. OVCAR-8	0.6	0.7
Stomach	0.9	0.8	Ovarian ca. IGROV-1	0.4	0.5
Small intestine	1.7	1.5	Ovarian ca. (ascites) SK-OV-3	0.0	0.1
Colon ca. SW480	0.1	0.1	Uterus	1.1	1.1
Colon ca.* SW620 (SW480 met)	0.1	0.1	Placenta	1.2	1.1
Colon ca. HT29	0.0	0.0	Prostate	0.7	0.4
Colon ca. HCT-116	2.7	2.6	Prostate ca.* (bone met) PC-3	0.0	0.0
Colon ca. CaCo-2	0.2	0.2	Testis	1.4	1.7
Colon ca. Tissue (ODO3866)	0.4	0.3	Melanoma Hs688(A).T	0.0	0.0
Colon ca. HCC-2998	0.1	0.1	Melanoma* (met) Hs688(B).T	0.0	0.0
Gastric ca.* (liver met) NCI-N87	0.2	0.2	Melanoma UACC-62	3.0	3.3
Bladder	0.9	1.0	Melanoma M14	0.4	0.7
Trachea	0.5	0.4	Melanoma LOX IMVI	0.0	0.0
Kidney	0.9	1.4	Melanoma* (met) SK-MEL-5	1.0	0.9
Kidney (fetal)	3.9	3.6			

Table BDF. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag07Gpcr, Run 181981925	Tissue Name	Rel. Exp.(%) Ag07Gpcr, Run 181981925
Secondary Th1 act	0.0	HUVEC IL-1beta	4.6
Secondary Th2 act	0.0	HUVEC IFN gamma	3.1
Secondary Tr1 act	1.1	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	2.1
Secondary Th2 rest	0.0	HUVEC IL-11	1.9
Secondary Tr1 rest	0.0	Lung Microvascular EC none	31.9
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	7.1
Primary Th2 act	0.0	Microvascular Dermal EC none	57.0
Primary Tr1 act	2.0	Microsvasular Dermal EC TNFalpha + IL-1beta	34.2
Primary Th1 rest	1.5	Bronchial epithelium TNFalpha + ILlbeta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	1.7
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	1.7
CD45RA CD4 lymphocyte act	1.1	Coronery artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronery artery SMC TNFalpha + IL-1beta	0.9
CD8 lymphocyte act	0.0	Astrocytes rest	1.2
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	6.4
Secondary CD8 lymphocyte act	1.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	2.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.7
LAK cells rest	6.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.9
LAK cells IL-2	0.0	Liver cirrhosis	9.4

LAK cells IL-2+IL-12	0.0	NCI-H292 none	1.1
LAK cells IL-2+IFN gamma	0.1	NCI-H292 IL-4	0.9
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.9
LAK cells PMA/ionomycin	1.1	NCI-H292 IL-13	1.9
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.9
Two Way MLR 3 day	0.0	HPAEC none	0.0
Two Way MLR 5 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
Two Way MLR 7 day	2.4	Lung fibroblast none	0.0
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	1.7
PBMC PWM	0.0	Lung fibroblast IL-4	1.1
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	2.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.2	Dermal fibroblast CCD1070 rest	4.8
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	1.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	1.7	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	35.6	Dermal fibroblast IL-4	1.8
Dendritic cells LPS	30.6	Dermal Fibroblasts rest	1.8
Dendritic cells anti-CD40	31.0	Neutrophils TNFa+LPS	2.2
Monocytes rest	0.0	Neutrophils rest	0.7
Monocytes LPS	4.2	Colon	8.5
Macrophages rest	28.3	Lung	100.0
Macrophages LPS	1.3	Thymus	11.2
HUVEC none	0.0	Kidney	77.4
HUVEC starved	3.3		

<u>Table BDG</u>. Panel CNS_1

Tissue Name	Rel. Exp.(%) Gpcr07, Run 182328460	Tissue Name	Rel. Exp.(%) Gpcr07, Run 182328460
BA4 Control	30.8	BA17 PSP	35.8
BA4 Control2	70.2	BA17 PSP2	11.2
BA4 Alzheimer's2	7.1	Sub Nigra Control	11.3
BA4 Parkinson's	23.8	Sub Nigra Control2	2.4
BA4 Parkinson's2	49.7	Sub Nigra Alzheimer's2	5.2
BA4 Huntington's	21.3	Sub Nigra Parkinson's2	11.7
BA4 Huntington's2	17.0	Sub Nigra Huntington's	16.5
BA4 PSP	10.1	Sub Nigra Huntington's2	6.2
BA4 PSP2	38.4	Sub Nigra PSP2	2.8
BA4 Depression	34.2	Sub Nigra Depression	4.0
BA4 Depression2	10.4	Sub Nigra Depression2	3.8
BA7 Control	33.0	Glob Palladus Control	3.0
BA7 Control2	30.4	Glob Palladus Control2	6.3
BA7 Alzheimer's2	9.0	Glob Palladus Alzheimer's	5.2
BA7 Parkinson's	11.7	Glob Palladus Alzheimer's2	4.6
BA7 Parkinson's2	17.2	Glob Palladus Parkinson's	32.8
BA7 Huntington's	36.3	Glob Palladus Parkinson's2	4.3
BA7 Huntington's2	21.8	Glob Palladus PSP	2.4
BA7 PSP	35.8	Glob Palladus PSP2	5.7
BA7 PSP2	23.7	Glob Palladus Depression	3.7
BA7 Depression	10.4	Temp Pole Control	21.6
BA9 Control	29.3	Temp Pole Control2	81.2
BA9 Control2	100.0	Temp Pole Alzheimer's	6.4

BA9 Alzheimer's	7.1	Temp Pole Alzheimer's2	16.0
BA9 Alzheimer's2	20.3	Temp Pole Parkinson's	29.5
BA9 Parkinson's	36.6	Temp Pole Parkinson's2	27.0
BA9 Parkinson's2	39.8	Temp Pole Huntington's	33.0
BA9 Huntington's	40.1	Temp Pole PSP	7.1
BA9 Huntington's2	17.3	Temp Pole PSP2	10.4
BA9 PSP	19.9	Temp Pole Depression2	12.1
BA9 PSP2	8.4	Cing Gyr Control	49.0
BA9 Depression	15.9	Cing Gyr Control2	76.3
BA9 Depression2	12.9	Cing Gyr Alzheimer's	16.8
BA17 Control	40.1	Cing Gyr Alzheimer's2	17.1
BA17 Control2	77.4	Cing Gyr Parkinson's	23.5
BA17 Alzheimer's2	11.9	Cing Gyr Parkinson's2	17.7
BA17 Parkinson's	29.3	Cing Gyr Huntington's	40.6
BA17 Parkinson's2	26.4	Cing Gyr Huntington's2	12.2
BA17 Huntington's	21.8	Cing Gyr PSP	11.8
BA17 Huntington's2	18.8	Cing Gyr PSP2	6.3
BA17 Depression	15.5	Cing Gyr Depression	12.5
BA17 Depression2	28.5	Cing Gyr Depression2	15.2

CNS_neurodegeneration_v1.0 Summary: Ag07Gpcr/ Gpcr07 Two runs with the same probe and primer set produce results that are in excellent agreement. This profile confirms the expression of this gene at moderate levels in the brain. This gene appears to be slightly down-regulated in the temporal cortex of Alzheimer's disease patients. Therefore, up-regulation of this gene or its protein product, or treatment with specific agonists for this receptor may be of use in reversing the dementia, memory loss, and neuronal death associated with this disease.

Panel 1 Summary: Gpcr07 Highest expression of this gene is seen in the hippocampus (CT=23), with high levels of detection seen in all regions of the CNS

examined. This gene encodes a leucine-rich repeat protein. Leucine rich repeats (LRR) mediate reversible protein-protein interactions and have diverse cellular functions, including cellular adhesion and signaling. Several of these proteins, such as connectin, slit, chaoptin, and Toll have pivotal roles in neuronal development in Drosophila and may play significant

5   but distinct roles in neural development and in the adult nervous system of humans (Ref. 1). In Drosophilia, the LRR region of axon guidance proteins has been shown to be critical for their function (especially in axon repulsion). Since the leucine-rich-repeat protein encoded by this gene shows high expression in the cerebral cortex, it is an excellent candidate neuronal guidance protein for axons, dendrites and/or growth cones in general. Therefore,

10   therapeutic modulation of the levels of this protein, or possible signaling via this protein, may be of utility in enhancing/directing compensatory synaptogenesis and fiber growth in the CNS in response to neuronal death (stroke, head trauma), axon lesion (spinal cord injury), or neurodegeneration (Alzheimer's, Parkinson's, Huntington's, vascular dementia or any neurodegenerative disease).

15   Moderate to high levels of expression are also seen in cell lines derived from kidney, breast, colon, melanoma, ovarian cancer, lung cancer, and brain cancer. Therefore, therapeutic modulation of the expression or function of this gene product may be effective in the treatment of these cancers.

          Among metabolically relevant tissues, this gene expression is seen in skeletal

20   muscle, thyroid, pancreas, adrenal, heart, adult and fetal liver, and pituitary gland. This observation suggests that therapeutic modulation may aid the treatment of metabolic diseases such as obesity and diabetes as well as neuroendocrine disorders. Glycoprotein hormones influence the development and function of the ovary, testis and thyroid by binding to specific high-affinity receptors. The extracellular domains of these receptors are

25   members of the leucine-rich repeat (LRR) protein superfamily and are responsible for the high-affinity binding.

          In addition, this gene is expressed at much higher levels in fetal kidney tissue (CT=24) when compared to expression in the adult counterpart (CT=28). Thus, expression of this gene may be used to differentiate between the fetal and adult source of this tissue.

30   References:

1. Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H., Hendrickson

W.A., el Tayar N. (1995) Structure 3: 1341-1353.

2. Battye R., Stevens A., Perry R.L., Jacobs J.R. (2001) J. Neurosci. 21: 4290-4298.

3. Itoh A., Miyabayashi T., Ohno M., Sakano S. 1998 Brain Res. Mol. Brain Res.

5   62: 175-186.

Panel 1.2 Summary: Ag07Gpcr /Gpcr07 Two runs with the same probe and primer
set produce results that are in excellent agreement. Highest expression of this gene is seen in
the cerebral cortex (CTs=21-22). High levels of expression are seen throughout the CNS,
consistent with Panel 1.

10   **Panel 4.1D Summary:** Ag07Gpcr Highest expression of this gene is seen in the
lung (CT=29.5). Moderate expression is also seen in the kidney, treated and untreated lung
and microvascular dermal endothelial cells, treated and untreated dendritic cells, and
macrophages. Therefore, therapeutic modulation of this gene may be used for the treatment
of autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel

15   disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

Panel CNS_1 Summary: Gpcr07 This panel confirms the expression of this gene
at high levels in the brain. See Panels 1 and CNS_neurodegeneration_v1.0 for discussion of
this gene in the central nervous system.

BE. CG99777-02: CD30 LIGAND-LIKE PROTEIN.

20   Expression of gene CG99777-02 was assessed using the primer-probe sets Ag6623,
Ag6747 and Ag6919, described in Tables BEA, BEB and BEC. Results of the RTQ-PCR
runs are shown in Tables BED, BEE and BEF. Note that CG99777-02 represents a full-
length physical clone.

Table BEA. Probe Name Ag6623

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-agaaagcgcctctctaccatac-3'	22	745	786
Probe	TET-5'-tatttcatccctccaaacacttgggc-3'-TAMRA	26	769	787

| Reverse | 5'-
gaggagaatccttcttggtctaaa-
3' | 24 | 806 | 788 |

Table BEB. Probe Name Ag6747

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-aaaggagtggcaaagcatct-3'	20	320	789
Probe	TET-5'- catggagaatgccatctttgttccaa -3'-TAMRA	26	358	790
Reverse	5'-ccagattcccatcctgatatc- 3'	21	390	791

Table BEC. Probe Name Ag6919

Primers	Sequences	Length	Start Position	SEQ ID No
Forward	5'-cctcaaaggagtggcaaagc-3'	20	316	792
Probe	TET-5'- caaaaccaagttgtcttggaacaaagatggcat tctcc-3'-TAMRA	38	343	793
Reverse	5'-ccagattcccatcctgatatctga-3'	24	387	794

Table BED. AI_comprehensive panel_v1.0

Tissue Name	Rel. Exp.(%) Ag6919, Run 308380234	Tissue Name	Rel. Exp.(%) Ag6919, Run 308380234
110967 COPD-F	6.9	112427 Match Control Psoriasis-F	10.0
110980 COPD-F	9.0	112418 Psoriasis-M	3.5
110968 COPD-M	7.0	112723 Match Control Psoriasis-M	2.7
110977 COPD-M	13.0	112419 Psoriasis-M	8.8
110989 Emphysema-F	7.8	112424 Match Control Psoriasis-M	3.3
110992 Emphysema-F	4.5	112420 Psoriasis-M	17.9
110993 Emphysema-F	3.4	112425 Match Control Psoriasis-M	9.6
110994 Emphysema-F	2.6	104689 (MF) OA Bone-Backus	50.3

110995 Emphysema-F	7.1	104690 (MF) Adj "Normal" Bone-Backus	27.9
110996 Emphysema-F	1.3	104691 (MF) OA Synovium-Backus	47.3
110997 Asthma-M	3.3	104692 (BA) OA Cartilage-Backus	0.0
111001 Asthma-F	11.3	104694 (BA) OA Bone-Backus	32.8
111002 Asthma-F	9.9	104695 (BA) Adj "Normal" Bone-Backus	27.2
111003 Atopic Asthma-F	8.8	104696 (BA) OA Synovium-Backus	82.4
111004 Atopic Asthma-F	8.0	104700 (SS) OA Bone-Backus	30.6
111005 Atopic Asthma-F	3.8	104701 (SS) Adj "Normal" Bone-Backus	40.9
111006 Atopic Asthma-F	0.8	104702 (SS) OA Synovium-Backus	66.4
111417 Allergy-M	4.4	117093 OA Cartilage Rep7	6.3
112347 Allergy-M	0.0	112672 OA Bone5	11.0
112349 Normal Lung-F	0.0	112673 OA Synovium5	5.8
112357 Normal Lung-F	6.7	112674 OA Synovial Fluid cells5	5.1
112354 Normal Lung-M	3.5	117100 OA Cartilage Rep14	2.8
112374 Crohns-F	4.7	112756 OA Bone9	3.2
112389 Match Control Crohns-F	8.2	112757 OA Synovium9	2.3
112375 Crohns-F	3.3	112758 OA Synovial Fluid Cells9	6.8
112732 Match Control Crohns-F	50.0	117125 RA Cartilage Rep2	7.1
112725 Crohns-M	1.9	113492 Bone2 RA	16.5
112387 Match Control Crohns-M	3.7	113493 Synovium2 RA	5.3
112378 Crohns-M	0.2	113494 Syn Fluid Cells RA	6.0

112390 Match Control Crohns-M	6.7	113499 Cartilage4 RA	9.9
112726 Crohns-M	12.6	113500 Bone4 RA	5.5
112731 Match Control Crohns-M	5.1	113501 Synovium4 RA	5.8
112380 Ulcer Col-F	2.3	113502 Syn Fluid Cells4 RA	6.2
112734 Match Control Ulcer Col-F	**100.0**	113495 Cartilage3 RA	7.8
112384 Ulcer Col-F	6.8	113496 Bone3 RA	9.5
112737 Match Control Ulcer Col-F	4.0	113497 Synovium3 RA	7.5
112386 Ulcer Col-F	4.0	113498 Syn Fluid Cells3 RA	11.3
112738 Match Control Ulcer Col-F	9.2	117106 Normal Cartilage Rep20	0.8
112381 Ulcer Col-M	0.2	113663 Bone3 Normal	0.0
112735 Match Control Ulcer Col-M	0.8	113664 Synovium3 Normal	0.0
112382 Ulcer Col-M	7.3	113665 Syn Fluid Cells3 Normal	0.1
112394 Match Control Ulcer Col-M	1.4	117107 Normal Cartilage Rep22	1.3
112383 Ulcer Col-M	4.8	113667 Bone4 Normal	1.8
112736 Match Control Ulcer Col-M	3.9	113668 Synovium4 Normal	3.0
112423 Psoriasis-F	5.0	113669 Syn Fluid Cells4 Normal	4.7

Table BEE. General_screening_panel_v1.6

Tissue Name	Rel. Exp.(%) Ag6919, Run 278388682	Tissue Name	Rel. Exp.(%) Ag6919, Run 278388682
Adipose	23.7	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	16.4
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.8
Melanoma* M14	0.0	Gastric ca. KATO III	0.0

Melanoma* LOXIMVI	1.4	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	2.6	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	5.2	Colon ca. CaCo-2	2.4
Placenta	5.7	Colon cancer tissue	15.5
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	15.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	4.3
Ovarian ca. IGROV-1	0.0	Stomach Pool	5.6
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	2.6
Ovary	9.9	Fetal Heart	1.4
Breast ca. MCF-7	0.0	Heart Pool	2.8
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	8.7
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	1.7
Breast ca. MDA-N	0.0	Spleen Pool	11.5
Breast Pool	7.3	Thymus Pool	46.3
Trachea	12.7	CNS cancer (glio/astro) U87-MG	2.2
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	15.5	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0

Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	4.7	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	2.4
Lung ca. NCI-H526	100.0	Brain (cerebellum)	1.8
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	1.7
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	1.0
Fetal Liver	5.6	Brain (whole)	1.7
Liver ca. HepG2	0.0	Spinal Cord Pool	4.3
Kidney Pool	13.9	Adrenal Gland	5.2
Fetal Kidney	3.4	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	1.8
Renal ca. A498	0.0	Thyroid (female)	0.8
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	1.7

Table BEF. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag6747, Run 277641366	Rel. Exp.(%) Ag6919, Run 306067437	Tissue Name	Rel. Exp.(%) Ag6747, Run 277641366	Rel. Exp.(%) Ag6919, Run 306067437
Secondary Th1 act	8.1	8.1	HUVEC IL-1beta	0.1	0.0
Secondary Th2 act	12.3	17.6	HUVEC IFN gamma	0.0	0.0
Secondary Tr1 act	3.3	5.1	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	3.8	3.4	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	4.0	3.9	HUVEC IL-11	1.4	0.0

Secondary Tr1 rest	6.0	7.1	Lung Microvascular EC none	0.0	0.0
Primary Th1 act	47.3	9.7	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0
Primary Th2 act	**100.0**	59.5	Microvascular Dermal EC none	0.0	0.0
Primary Tr1 act	82.4	**100.0**	Microsvasular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	1.3	1.2	Bronchial epithelium TNFalpha + IL1beta	0.0	0.0
Primary Th2 rest	1.6	1.7	Small airway epithelium none	0.0	0.0
Primary Tr1 rest	0.5	0.5	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	6.0	6.8	Coronery artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	12.4	19.1	Coronery artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	1.3	1.1	Astrocytes rest	0.0	0.0
Secondary CD8 lymphocyte rest	1.9	1.2	Astrocytes TNFalpha + IL-1beta	0.0	0.0
Secondary CD8 lymphocyte act	1.0	0.4	KU-812 (Basophil) rest	0.0	0.0
CD4 lymphocyte none	3.1	2.4	KU-812 (Basophil) PMA/ionomycin	0.0	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	2.3	3.0	CCD1106 (Keratinocytes) none	0.0	0.0
LAK cells rest	3.6	3.3	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	1.2	1.2	Liver cirrhosis	0.2	0.3
LAK cells IL-2+IL-12	0.3	0.3	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	1.8	2.1	NCI-H292 IL-4	0.0	0.0

LAK cells IL-2+ IL-18	0.8	0.9	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	12.9	18.7	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	6.4	5.4	NCI-H292 IFN gamma	0.0	0.0
Two Way MLR 3 day	2.1	1.6	HPAEC none	0.0	0.0
Two Way MLR 5 day	0.4	0.6	HPAEC TNF alpha + IL-1 beta	0.2	0.0
Two Way MLR 7 day	0.6	0.5	Lung fibroblast none	0.0	0.0
PBMC rest	1.1	2.1	Lung fibroblast TNF alpha + IL-1 beta	0.0	0.0
PBMC PWM	0.7	0.3	Lung fibroblast IL-4	0.0	0.0
PBMC PHA-L	1.0	1.2	Lung fibroblast IL-9	0.0	0.0
Ramos (B cell) none	3.6	4.7	Lung fibroblast IL-13	0.0	0.0
Ramos (B cell) ionomycin	15.4	15.1	Lung fibroblast IFN gamma	0.0	0.0
B lymphocytes PWM	2.6	3.0	Dermal fibroblast CCD1070 rest	0.0	0.0
B lymphocytes CD40L and IL-4	4.8	4.1	Dermal fibroblast CCD1070 TNF alpha	6.3	4.6
EOL-1 dbcAMP	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
EOL-1 dbcAMP PMA/ionomycin	0.1	0.0	Dermal fibroblast IFN gamma	0.0	0.0
Dendritic cells none	1.6	2.7	Dermal fibroblast IL-4	0.0	0.0
Dendritic cells LPS	1.3	1.2	Dermal Fibroblasts rest	0.0	0.0
Dendritic cells anti-CD40	1.1	1.4	Neutrophils TNFa+LPS	3.7	4.9
Monocytes rest	2.2	3.3	Neutrophils rest	2.1	3.3
Monocytes LPS	9.4	9.4	Colon	0.1	0.0
Macrophages rest	1.1	0.3	Lung	0.1	0.0
Macrophages LPS	0.5	0.5	Thymus	1.5	3.0
HUVEC none	0.0	0.0	Kidney	0.1	0.0

HUVEC starved	0.0	0.0			

AI_comprehensive panel_v1.0 Summary: Ag6919 Highest expression of this gene is seen in a normal tissue adjacent to ulcerative colitis (CT=29.5). This gene is widely expressed in this panel, with moderate levels of expression in a cluster of OA samples. Thus, expression of this gene could be used to differentiate between the OA samples and other samples on this panel, and as a marker of OA. Furthermore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of OA.

General_screening_panel_v1.6 Summary: Ag6919 Expression of this gene is restricted to a sample derived from a lung cancer cell line and from the thymus(CTs=33-34). Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of lung cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung cancer.

Panel 4.1D Summary: Ag6747/Ag6919 Expression is highest in acutely activated T cells (CTs=25-30). This gene is expressed at higher levels during primary activation of Th2 and Tr1 cells. Thus, this gene may be important for early Th2 cell differentiation and Th2 related immune disorders such as asthma. This gene encodes a protein with homology to CD30-L, a member of the tumor necrosis factor receptor superfamily expressed on the surface of activated T cells. Thus based on this expression profile, therapeutics designed with the protein encoded by this transcript could be important in the regulation of T cell function. In addition, therapeutic regulation of the transcript or the protein encoded by the transcript could be important in immune modulation and in the treatment of T cell-mediated diseases such as asthma, arthritis, psoriasis, inflammatory bowel disease, and lupus.

Ag6623 Expression of this gene is low/undetectable in all samples on this panel (CTs>35).

Example D: Identification of Single Nucleotide Polymorphisms in NOVX nucleic acid sequences

Variant sequences are also included in this application. A variant sequence can include a single nucleotide polymorphism (SNP). A SNP can, in some instances, be

referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP originates as a cDNA. A SNP can arise in several ways. For example, a SNP may be due to a substitution of one nucleotide for another at the polymorphic site. Such a substitution can be either a transition or a transversion. A SNP can also arise from a deletion of a nucleotide

5   or an insertion of a nucleotide, relative to a reference allele. In this case, the polymorphic site is a site at which one allele bears a gap with respect to a particular nucleotide in another allele. SNPs occurring within genes may result in an alteration of the amino acid encoded by the gene at the position of the SNP. Intragenic SNPs may also be silent, when a codon including a SNP encodes the same amino acid as a result of the redundancy of the genetic

10   code. SNPs occurring outside the region of a gene, or in an intron within a gene, do not result in changes in any amino acid sequence of a protein but may result in altered regulation of the expression pattern. Examples include alteration in temporal expression, physiological response regulation, cell type expression regulation, intensity of expression, and stability of transcribed message.

15   SeqCalling assemblies produced by the exon linking process were selected and extended using the following criteria. Genomic clones having regions with 98% identity to all or part of the initial or extended sequence were identified by BLASTN searches using the relevant sequence to query human genomic databases. The genomic clones that resulted were selected for further analysis because this identity indicates that these clones contain the

20   genomic locus for these SeqCalling assemblies. These sequences were analyzed for putative coding regions as well as for similarity to the known DNA and protein sequences. Programs used for these analyses include Grail, Genscan, BLAST, HMMER, FASTA, Hybrid and other relevant programs.

Some additional genomic regions may have also been identified because selected

25   SeqCalling assemblies map to those regions. Such SeqCalling sequences may have overlapped with regions defined by homology or exon prediction. They may also be included because the location of the fragment was in the vicinity of genomic regions identified by similarity or exon prediction that had been included in the original predicted sequence. The sequence so identified was manually assembled and then may have been

30   extended using one or more additional sequences taken from CuraGen Corporation's human SeqCalling database. SeqCalling fragments suitable for inclusion were identified by the

CuraTools™ program SeqExtend or by identifying SeqCalling fragments mapping to the appropriate regions of the genomic clones analyzed.

The regions defined by the procedures described above were then manually integrated and corrected for apparent inconsistencies that may have arisen, for example,

5 from miscalled bases in the original fragments or from discrepancies between predicted exon junctions, EST locations and regions of sequence similarity, to derive the final sequence disclosed herein. When necessary, the process to identify and analyze SeqCalling assemblies and genomic clones was reiterated to derive the full length sequence (Alderborn *et al.*, Determination of Single Nucleotide Polymorphisms by Real-time Pyrophosphate

10 DNA Sequencing. Genome Research. 10 (8) 1249-1265, 2000).

Variants are reported individually but any combination of all or a select subset of variants are also included as contemplated NOVX embodiments of the invention.

NOV1b SNP Data (CG108440-02)

Three polymorphic variants of NOV1b have been identified and are shown in Table

15 41A.

Table 41A. NOV1b SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380440	1921	C	T	639	Ser	Phe
13378327	4730	A	G	1575	Glu	Glu
13378325	6395	T	C	2130	Tyr	Tyr

NOV4a SNP Data (CG1344340-01)

One polymorphic variant of NOV4a has been identified and is shown in Table 41B.

Table 41B. NOV4a SNP Data

Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified

13380480	652	G	A	144	Trp	End

NOV8b SNP Data (CG137793-02)

Twenty polymorphic variants of NOV8b have been identified and are shown in

Table 41C.

Table 41C. NOV8b SNP Data						
Variant	**Nucleotides**			**Amino Acids**		
	Position	Initial	Modified	Position	Initial	Modified
13380443	52	T	C	9	Thr	Thr
13380444	65	G	A	14	Ala	Thr
13380445	80	G	A	19	Ala	Thr
13380446	146	A	G	41	Ile	Val
13380447	168	C	T	48	Thr	Ile
13380448	190	T	C	55	Asn	Asn
13380449	211	C	T	62	Thr	Thr
13380450	234	T	C	70	Leu	Pro
13380451	241	A	G	72	Glu	Glu
13380452	242	G	T	73	Glu	End
13380459	355	T	C	110	Gly	Gly
13380460	486	C	T	154	Thr	Ile
13380461	497	G	A	158	Ala	Thr
13380462	579	T	C	185	Ile	Thr
13380463	586	T	C	187	Thr	Thr
13380464	597	T	C	191	Val	Ala
13380465	609	T	C	195	Leu	Ser

13380466	649	C	A	208	Asn	Lys
13380467	665	A	G	214	Asn	Asp
13380468	694	A	G	0		

NOV16a SNP Data (CG138751-01)

Two polymorphic variants of NOV16a have been identified and are shown in Table 41D.

Table 41D. SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380684	70	T	C	4	Ser	Pro
13380685	411	C	T	117	Tyr	Tyr

5

NOV17b SNP Data (CG139062-02)

Five polymorphic variants of NOV17b have been identified and are shown in Table 41E.

Table 41E. NOV17b SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380469	680	G	A	89	Gly	Gly
13380470	801	A	G	130	Arg	Gly
13380471	1178	T	C	255	Tyr	Tyr
13380475	2684	C	T	757	Tyr	Tyr
13380476	3945	G	T	0		

NOV20a SNP Data (CG140305-01)

Two polymorphic variants of NOV20a have been identified and are shown in Table

5 41F.

Table 41F. NOV20a SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380503	218	G	T	57	Gly	Val
13380501	404	T	C	119	Val	Ala

NOV22a SNP Data (CG140843-01)

One polymorphic variant of NOV22a has been identified and is shown in Table

41G.

10

Table 41G. NOV22a SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380504	217	A	G	57	Pro	Pro

NOV23a SNP Data (CG141540-01)

Six plymorphic variants of NOV23a have been identified and are shown in Table

15 41H.

Table 41H. NOV23a SNP Data		
Variant .	Nucleotides .	Amino Acids .

	Position	Initial	Modified	Position	Initial	Modified
13380496	132	A	G	22	Thr	Thr
13377809	184	A	G	40	Arg	Gly
13377810	227 .	C	T	54	Pro	Leu
13378253	258	C	A	64	Arg	Arg
13377812	823	T	C	253	Trp	Arg
13378251	1044	G	A	326	Thr	Thr

NOV24a SNP Data (CG14580-01)

Two polymorphic variants of NOV24a have been identified and are shown in Table 41I.

Table 41I. NOV24a SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380498	197	G	A	46	Gly	Glu
13380497 .	1693	G	A	545	Ala	Thr

5

NOV26a SNP Data (CG142003-01)

One polymorphic variant of NOV26a has been identified and is shown in Table 41J.

Table 41J. NOV26a SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380544	375	G	A	125	Val	Met

10

NOV29c SNP Data (CG171681-02)

Two polymorphic variants of NOV29c have been identified and are shown in Table 41K.

Table 41K. NOV29c SNP Data					
Variant	**Nucleotides**			**Amino Acids**		
	Position	Initial	Modified	Position	Initial	Modified
13380521	361	A	G	96	Lys	Arg
13380522	1646	G	C	0		

5   **NOV32a SNP Data (CG52423-01)**

Twenty polymorphic variants of NOV32a have been identified and are shown in Table 41L.

Table 41L. NOV32a SNP Data					
Variant	**Nucleotides**			**Amino Acids**		
	Position	Initial	Modified	Position	Initial	Modified
13380557	26	C	T	0		
13380556	54	A	G	1	Met	Val
13380555	60	G	A	3	Ala	Thr
13380545	357	A	G	102	Asn	Asp
13380546	562	A	G	170	Asn	Ser
13380547	739	A	G	229	Glu	Gly
13380548	760	A	G	236	Gln	Arg
13380549	774	C	T	241	Gln	End
13380550	796	A	G	248	Asp	Gly
13380551	843	A	G	264	Ile	Val

13380552	868	T	C	272	Leu	Pro
13380553	892	T	C	280	Leu	Pro
13380554	893	G	A	280	Leu	Leu
13380542	1066	A	G	338	Gln	Arg
13380558	1073	G	A	340	Ala	Ala
13374369	1133	C	G	360	Ser	Ser
13380559	1151	G	A	366	Ala	Ala
13380560	1288	A	G	412	Lys	Arg
13380515	1303	T	C	417	Met	Thr
13374368	1357	C	T	435	Ala	Val

NOV34b SNP Data (CG55698-02)

Four polymorphic variants of NOV34b have been identified and are shown in Table

5   41M.

Table 41M. NOV34b SNP Data						
Variant	**Nucleotides**			**Amino Acids**		
	Position	Initial	Modified	Position	Initial	Modified
13380563	170	G	A	52	Val	Met
13380564	210	A	G	65	Asp	Gly
13380565	218	C	T	68	Arg	Cys
13380566	249	C	T	0		

NOV35c SNP Data (CG55832-02)

Twelve polymorphic variants of NOV35c have been identified and are shown in
Table 41N.

Table 41N. NOV35c SNP Data						
Variant	**Nucleotides**			**Amino Acids**		
	Position	Initial	Modified	Position	Initial	Modified
13380671	330	A	G	92	Val	Val
13380672	638	A	G	195	His	Arg
13380673	750	G	A	232	Val	Val
13380674	1260	T	C	402	Cys	Cys
13378289	2090	G	A	679	Arg	Gln
13380675	2100	G	A	682	Glu	Glu
13380676	3342	A	G	1096	Thr	Thr
13380677	3813	A	G	1253	Arg	Arg
13380678	4118	C	T	1355	Thr	Met
13378291	4162	C	G	1370	Gln	Glu
13380705	4397	T	C	1448	Val	Ala
13380704	5269	A	G	0		

5

NOV37a SNP Data (CG88634-01)

Two polymorphic variants of NOV37a have been identified and are shown in Table
41O.

Table 41O. NOV37a SNP Data		
Variant	**Nucleotides**	**Amino Acids**

	Position	Initial	Modified	Position	Initial	Modified
13380706	165	T	C	22	Leu	Pro
13380707	272	A	C	58	Lys	Gln

NOV38a SNP Data (CG97012-01)

Two polymorphic variants of NOV38a have been identified and are shown in Table 41P.

Table 41P. NOV38a SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13380698	828	G	A	276	Gln	Gln
13380699	1271	A	G	424	Glu	Gly

5

NOV39a SNP Data (CG99754-01)

Six polymorphic variants of NOV39a have been identified and are shown in Table 41Q.

Table 41Q. NOV39a SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13374727	314	T	C	100	Ile	Thr
13374728	362	G	A	116	Arg	Gln
13380709	545	C	T	177	Ser	Phe
13380710	711	G	C	232	Leu	Leu
13380711	1355	C	T	447	Pro	Leu

13380712	1886	C	T	0		

NOV40b SNP Data (CG99777-02)

Three polymorphic variants of NOV40b have been identified and are shown in Table 41R.

5

Table 41R. NOV40b SNP Data						
Variant	Nucleotides			Amino Acids		
	Position	Initial	Modified	Position	Initial	Modified
13378112	466	A	G	126	Gln	Gln
13378113	498	A	G	137	Glu	Gly
13378114	641	G	A	185	Asp	Asn

NOV30b SAGE Expression Data

Construction of the mammalian expression vector pCEP4/Sec. The

10   oligonucleotide primers, pSec-V5-His Forward (CTCGTC CTCGAG GGT AAG CCT
ATC CCT AAC; SEQ ID NO:795) and the pSec-V5-His Reverse
(CTCGTCGGGCCCCTGATCAGCGGGTTTAAAC; SEQ ID NO:796), were designed to
amplify a fragment from thepcDNA3.1-V5His (Invitrogen, Carlsbad, CA) expression
vector. The PCR product was digested with XhoI and ApaI and ligated into the XhoI/ApaI

15   digestedpSecTag2 B vector (Invitrogen, Carlsbad CA). The correct structure of the resulting
vector, pSecV5His, was verified by DNA sequence analysis. The vector pSecV5His was
digested with PmeI and NheI, and the PmeI-NheI fragment was ligated into the
BamHI/Klenow and NheI treated vector pCEP4 (Invitrogen, Carlsbad, CA). The resulting
vector was named as pCEP4/Sec.

20   **Expression of CG51117-05 in human embryonic kidney 293 cells.** A 1.6 kb
BamHI-XhoI fragment containing the CG5117-05 sequence was subcloned into BamHI-
XhoI digested pCEP4/Sec to generate plasmid 163. The resulting plasmid 163 was

transfected into 293 cells using the LipofectaminePlus reagent following the manufacturer's

instructions (Gibco/BRL). The cell pellet and supernatant were harvested 72h post

transfection and examined for CG51117-05 expression by Western blot (reducing

conditions) using an anti-V5 antibody. Fig. 1 shows that CG51117-05 is expressed as an

5   approximately 66 kDa protein, secreted by 293 cells.

OTHER EMBODIMENTS

Although particular embodiments have been disclosed herein in detail, this has been

10   done by way of example for purposes of illustration only, and is not intended to be limiting

with respect to the scope of the appended claims, which follow. In particular, it is

contemplated by the inventors that various substitutions, alterations, and modifications may

be made to the invention without departing from the spirit and scope of the invention as

defined by the claims. The choice of nucleic acid starting material, clone of interest, or

15   library type is believed to be a matter of routine for a person of ordinary skill in the art with

knowledge of the embodiments described herein. Other aspects, advantages, and

modifications considered to be within the scope of the following claims. The claims

presented are representative of the inventions disclosed herein. Other, unclaimed inventions

are also contemplated. Applicants reserve the right to pursue such inventions in later

20   claims.

CLAIMS

What is claimed is:

1.   An isolated polypeptide comprising the mature form of an amino acid sequenced selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

2.   An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

3.   An isolated polypeptide comprising an amino acid sequence which is at least 95% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

4.   An isolated polypeptide, wherein the polypeptide comprises an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127.

5.   The polypeptide of claim 1 wherein said polypeptide is naturally occurring.

6.   A composition comprising the polypeptide of claim 1 and a carrier.

7.   A kit comprising, in one or more containers, the composition of claim 6.

8.   The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a human disease, the disease selected from a pathology associated

with the polypeptide of claim 1, wherein the therapeutic comprises the polypeptide of claim 1.

9.   A method for determining the presence or amount of the polypeptide of claim 1 in a sample, the method comprising:

        (a)   providing said sample;

        (b)   introducing said sample to an antibody that binds immunospecifically to the polypeptide; and

        (c)   determining the presence or amount of antibody bound to said polypeptide,

thereby determining the presence or amount of polypeptide in said sample.

10.   A method for determining the presence of or predisposition to a disease associated with altered levels of expression of the polypeptide of claim 1 in a first mammalian subject, the method comprising:

        a)   measuring the level of expression of the polypeptide in a sample from the first mammalian subject; and

        b)   comparing the expression of said polypeptide in the sample of step (a) to the expression of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, said disease,

wherein an alteration in the level of expression of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to said disease.

11.   A method of identifying an agent that binds to the polypeptide of claim 1, the method comprising:

        (a)   introducing said polypeptide to said agent; and

        (b)   determining whether said agent binds to said polypeptide.

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12.   The method of claim 11 wherein the agent is a cellular receptor or a downstream effector.

13.   A method for identifying a potential therapeutic agent for use in treatment of a pathology, wherein the pathology is related to aberrant expression or aberrant physiological interactions of the polypeptide of claim 1, the method comprising:

(a)   providing a cell expressing the polypeptide of claim 1 and having a property or function ascribable to the polypeptide;

(b)   contacting the cell with a composition comprising a candidate substance; and

(c)   determining whether the substance alters the property or function ascribable to the polypeptide;

whereby, if an alteration observed in the presence of the substance is not observed when the cell is contacted with a composition in the absence of the substance, the substance is identified as a potential therapeutic agent.

14.   A method for screening for a modulator of activity of or of latency or predisposition to a pathology associated with the polypeptide of claim 1, said method comprising:

(a)   administering a test compound to a test animal at increased risk for a pathology associated with the polypeptide of claim 1, wherein said test animal recombinantly expresses the polypeptide of claim 1;

(b)   measuring the activity of said polypeptide in said test animal after administering the compound of step (a); and

(c)   comparing the activity of said polypeptide in said test animal with the activity of said polypeptide in a control animal not administered said polypeptide, wherein a change in the activity of said polypeptide in said test animal relative to said control animal indicates the test compound is a

modulator activity of or latency or predisposition to, a pathology associated
with the polypeptide of claim 1.

15.   The method of claim 14, wherein said test animal is a recombinant test
animal that expresses a test protein transgene or expresses said transgene under the control
of a promoter at an increased level relative to a wild-type test animal, and wherein said
promoter is not the native gene promoter of said transgene.

16.   A method for modulating the activity of the polypeptide of claim 1, the
method comprising contacting a cell sample expressing the polypeptide of claim 1 with a
compound that binds to said polypeptide in an amount sufficient to modulate the activity of
the polypeptide.

17.   A method of treating or preventing a pathology associated with the
polypeptide of claim 1, the method comprising administering the polypeptide of claim 1 to a
subject in which such treatment or prevention is desired in an amount sufficient to treat or
prevent the pathology in the subject.

18.   The method of claim 17, wherein the subject is a human.

19.   A method of treating a pathological state in a mammal, the method
comprising administering to the mammal a polypeptide in an amount that is sufficient to
alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino
acid sequence at least 95% identical to a polypeptide comprising the amino acid sequence
selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and
127 or a biologically active fragment thereof.

20.   An isolated nucleic acid molecule comprising a nucleic acid sequence
selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1
and 127.

21.   The nucleic acid molecule of claim 20, wherein the nucleic acid molecule is
naturally occurring.

22.   A nucleic acid molecule, wherein the nucleic acid molecule differs by a
single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ
ID NO: 2n-1, wherein n is an integer between 1 and 127.

23.   An isolated nucleic acid molecule encoding the mature form of a polypeptide
having an amino acid sequence selected from the group consisting of SEQ ID NO:2n,
wherein n is an integer between 1 and 127.

24.   An isolated nucleic acid molecule comprising a nucleic acid selected from
the group consisting of 2n-1, wherein n is an integer between 1 and 127.

25.   The nucleic acid molecule of claim 20, wherein said nucleic acid molecule
hybridizes under stringent conditions to the nucleotide sequence selected from the group
consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 127, or a
complement of said nucleotide sequence.

26.   A vector comprising the nucleic acid molecule of claim 20.

27.   The vector of claim 26, further comprising a promoter operably linked to
said nucleic acid molecule.

28.   A cell comprising the vector of claim 26.

29.   An antibody that immunospecifically binds to the polypeptide of claim 1.

30.   The antibody of claim 29, wherein the antibody is a monoclonal antibody.

31.   The antibody of claim 29, wherein the antibody is a humanized antibody.

32.   A method for determining the presence or amount of the nucleic acid molecule of claim 20 in a sample, the method comprising:

        (a)   providing said sample;

        (b)   introducing said sample to a probe that binds to said nucleic acid molecule; and

        (c)   determining the presence or amount of said probe bound to said nucleic acid molecule,

    thereby determining the presence or amount of the nucleic acid molecule in said sample.

33.   The method of claim 32 wherein presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type.

34.   The method of claim 33 wherein the cell or tissue type is cancerous.

35.   A method for determining the presence of or predisposition to a disease associated with altered levels of expression of the nucleic acid molecule of claim 20 in a first mammalian subject, the method comprising:

a)   measuring the level of expression of the nucleic acid in a sample from the first mammalian subject; and

b)   comparing the level of expression of said nucleic acid in the sample of step (a) to the level of expression of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease;

wherein an alteration in the level of expression of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

36.   A method of producing the polypeptide of claim 1, the method comprising culturing a cell under conditions that lead to expression of the polypeptide, wherein said cell comprises a vector comprising an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127.

37.   The method of claim 36 wherein the cell is a bacterial cell.

38.   The method of claim 36 wherein the cell is an insect cell.

39.   The method of claim 36 wherein the cell is a yeast cell.

40.   The method of claim 36 wherein the cell is a mammalian cell.

41.   A method of producing the polypeptide of claim 2, the method comprising culturing a cell under conditions that lead to expression of the polypeptide, wherein said cell comprises a vector comprising an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127.

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42.   The method of claim 41 wherein the cell is a bacterial cell.

43.   The method of claim 41 wherein the cell is an insect cell.

44.   The method of claim 41 wherein the cell is a yeast cell.

45.   The method of claim 41 wherein the cell is a mammalian cell.

Fig. 1. NOV30b (CG51117-05) protein secreted by 293 cells.

Mw (kDa)
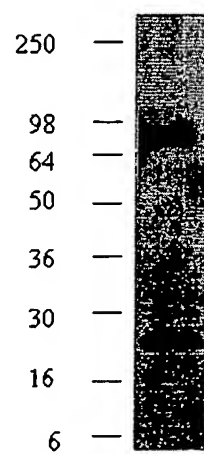
Fig. 2. NOV34b (CG55698-02) schematic diagram of colipase and tetra ehtylene glycol monooctyl ether inhibitor
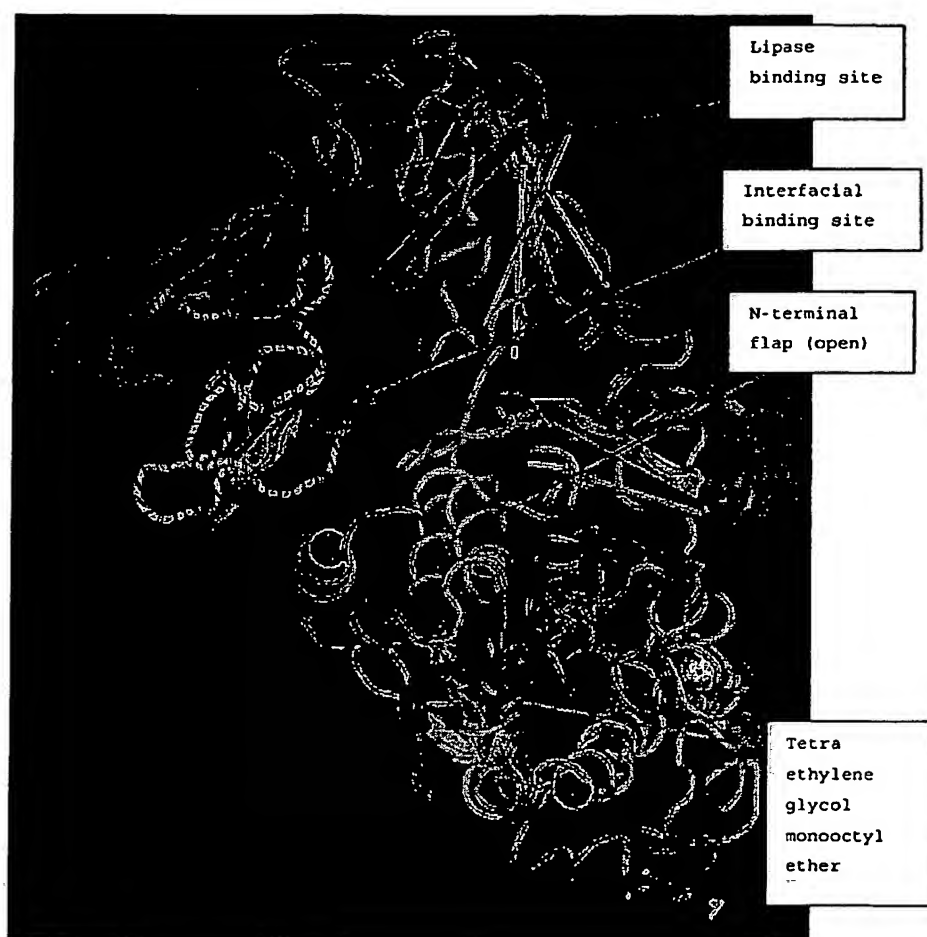
Fig. 3. Schematic diagram of interfacial binding site of colipase
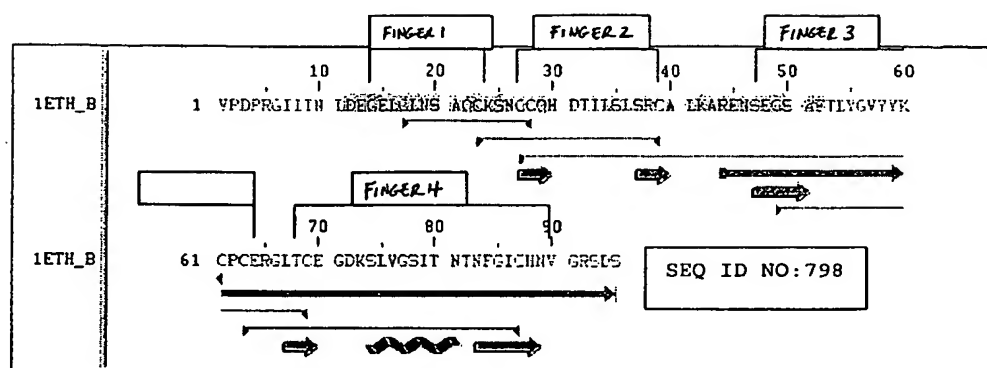
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(54) Title: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE

(57) Abstract:

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THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE

FIELD OF THE INVENTION

The present invention relates to novel polypeptides, and the nucleic acids encoding them, having properties related to stimulation of biochemical or physiological responses in a cell, a tissue, an organ or an organism. More particularly, the novel polypeptides are gene products of novel genes, or are specified biologically active fragments or derivatives thereof. Methods of use encompass diagnostic and prognostic assay procedures as well as methods of treating diverse pathological conditions.

BACKGROUND OF THE INVENTION

Eukaryotic cells are characterized by biochemical and physiological processes which under normal conditions are exquisitely balanced to achieve the preservation and propagation of the cells. When such cells are components of multicellular organisms such as vertebrates, or more particularly organisms such as mammals, the regulation of the biochemical and physiological processes involves intricate signaling pathways. Frequently, such signaling pathways involve extracellular signaling proteins, cellular receptors that bind the signaling proteins, and signal transducing components located within the cells.

Signaling proteins may be classified as endocrine effectors, paracrine effectors or autocrine effectors. Endocrine effectors are signaling molecules secreted by a given organ into the circulatory system, which are then transported to a distant target organ or tissue. The target cells include the receptors for the endocrine effector, and when the endocrine effector binds, a signaling cascade is induced. Paracrine effectors involve secreting cells and receptor cells in close proximity to each other, for example two different classes of cells in the same tissue or organ. One class of cells secretes the paracrine effector, which then reaches the second class of cells, for example by diffusion through the extracellular fluid. The second class of cells contains the receptors for the paracrine effector; binding of the effector results in induction of the signaling cascade that elicits the corresponding biochemical or physiological effect. Autocrine effectors are highly analogous to paracrine effectors, except that the same cell type that secretes the autocrine effector also contains the receptor. Thus the autocrine effector binds to receptors on the same cell, or on identical neighboring cells. The binding process then elicits the characteristic biochemical or physiological effect.

Signaling processes may elicit a variety of effects on cells and tissues including by way of nonlimiting example induction of cell or tissue proliferation, suppression of growth or proliferation, induction of differentiation or maturation of a cell or tissue, and suppression of differentiation or maturation of a cell or tissue.

Many pathological conditions involve dysregulation of expression of important effector proteins. In certain classes of pathologies the dysregulation is manifested as diminished or suppressed level of synthesis and secretion of protein effectors. In other classes of pathologies the dysregulation is manifested as increased or up-regulated

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level of synthesis and secretion of protein effectors. In a clinical setting a subject may be suspected of suffering from a condition brought on by altered or mis-regulated levels of a protein effector of interest. Therefore there is a need to assay for the level of the protein effector of interest in a biological sample from such a subject, and to compare the level with

5   that characteristic of a nonpathological condition. There also is a need to provide the protein effector as a product of manufacture. Administration of the effector to a subject in need thereof is useful in treatment of the pathological condition. Accordingly, there is a need for a method of treatment of a pathological condition brought on by a diminished or suppressed levels of the protein effector of interest. In addition, there is a need for a method

10   of treatment of a pathological condition brought on by a increased or up-regulated levels of the protein effector of interest.

Antibodies are multichain proteins that bind specifically to a given antigen, and bind poorly, or not at all, to substances deemed not to be cognate antigens. Antibodies are comprised of two short chains termed light chains and two long chains termed heavy chains.

15   These chains are constituted of immunoglobulin domains, of which generally there are two classes: one variable domain per chain, one constant domain in light chains, and three or more constant domains in heavy chains. The antigen-specific portion of the immunoglobulin molecules resides in the variable domains; the variable domains of one light chain and one heavy chain associate with each other to generate the antigen-binding

20   moiety. Antibodies that bind immunospecifically to a cognate or target antigen bind with high affinities. Accordingly, they are useful in assaying specifically for the presence of the antigen in a sample. In addition, they have the potential of inactivating the activity of the antigen.

Therefore there is a need to assay for the level of a protein effector of interest in a

25   biological sample from such a subject, and to compare this level with that characteristic of a nonpathological condition. In particular, there is a need for such an assay based on the use of an antibody that binds immunospecifically to the antigen. There further is a need to inhibit the activity of the protein effector in cases where a pathological condition arises from elevated or excessive levels of the effector based on the use of an antibody that binds

30   immunospecifically to the effector. Thus, there is a need for the antibody as a product of manufacture. There further is a need for a method of treatment of a pathological condition

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brought on by an elevated or excessive level of the protein effector of interest based on administering the antibody to the subject.

SUMMARY OF THE INVENTION

The invention is based in part upon the discovery of isolated polypeptides including
5 amino acid sequences selected from mature forms of the amino acid sequences selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127. The novel nucleic acids and polypeptides are referred to herein as NOVX, or NOV1, NOV2, NOV3, *etc.*, nucleic acids and polypeptides. These nucleic acids and polypeptides, as well as derivatives, homologs, analogs and fragments thereof, will hereinafter be
10 collectively designated as "NOVX" nucleic acid or polypeptide sequences.

The invention also is based in part upon variants of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, wherein any amino acid in the mature form is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of
15 the mature form are so changed. In another embodiment, the invention includes the amino acid sequences selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127. In another embodiment, the invention also comprises variants of the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, wherein any amino acid specified in the chosen sequence is
20 changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed. The invention also involves fragments of any of the mature forms of the amino acid sequences selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, or any other amino acid sequence selected from this group. The invention also comprises fragments from these groups in
25 which up to 15% of the residues are changed.

In another embodiment, the invention encompasses polypeptides that are naturally occurring allelic variants of the sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127. These allelic variants include amino acid sequences that are the translations of nucleic acid sequences differing by a single nucleotide
30 from nucleic acid sequences selected from the group consisting of SEQ ID NOS: 2n-1,

wherein n is an integer between 1 and 127. The variant polypeptide where any amino acid changed in the chosen sequence is changed to provide a conservative substitution.

In another embodiment, the invention comprises a pharmaceutical composition involving a polypeptide with an amino acid sequence selected from the group consisting of

5   SEQ ID NO:2n, wherein n is an integer between 1 and 127, and a pharmaceutically acceptable carrier. In another embodiment, the invention involves a kit, including, in one or more containers, this pharmaceutical composition.

In another embodiment, the invention includes the use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a human disease, the

10   disease being selected from a pathology associated with a polypeptide with an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, wherein said therapeutic is the polypeptide selected from this group.

In another embodiment, the invention comprises a method for determining the presence or amount of a polypeptide with an amino acid sequence selected from the group

15   consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, in a sample, the method involving providing the sample; introducing the sample to an antibody that binds immunospecifically to the polypeptide; and determining the presence or amount of antibody bound to the polypeptide, thereby determining the presence or amount of polypeptide in the sample.

20   In another embodiment, the invention includes a method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide with an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, in a first mammalian subject, the method involving measuring the level of expression of the polypeptide in a sample from the first mammalian

25   subject; and comparing the amount of the polypeptide in this sample to the amount of the polypeptide present in a control sample from a second mammalian subject known not to have, or not to be predisposed to, the disease, wherein an alteration in the expression level of the polypeptide in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

30   In another embodiment, the invention involves a method of identifying an agent that binds to a polypeptide with an amino acid sequence selected from the group consisting of

SEQ ID NO:2n, wherein n is an integer between 1 and 127, the method including introducing the polypeptide to the agent; and determining whether the agent binds to the polypeptide. The agent could be a cellular receptor or a downstream effector.

5   In another embodiment, the invention involves a method for identifying a potential therapeutic agent for use in treatment of a pathology, wherein the pathology is related to aberrant expression or aberrant physiological interactions of a polypeptide with an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, the method including providing a cell expressing the polypeptide of the invention and having a property or function ascribable to the polypeptide; contacting the

10   cell with a composition comprising a candidate substance; and determining whether the substance alters the property or function ascribable to the polypeptide; whereby, if an alteration observed in the presence of the substance is not observed when the cell is contacted with a composition devoid of the substance, the substance is identified as a potential therapeutic agent.

15   In another embodiment, the invention involves a method for screening for a modulator of activity or of latency or predisposition to a pathology associated with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, the method including administering a test compound to a test animal at increased risk for a pathology associated with the

20   polypeptide of the invention, wherein the test animal recombinantly expresses the polypeptide of the invention; measuring the activity of the polypeptide in the test animal after administering the test compound; and comparing the activity of the protein in the test animal with the activity of the polypeptide in a control animal not administered the polypeptide, wherein a change in the activity of the polypeptide in the test animal relative to

25   the control animal indicates the test compound is a modulator of latency of, or predisposition to, a pathology associated with the polypeptide of the invention. The recombinant test animal could express a test protein transgene or express the transgene under the control of a promoter at an increased level relative to a wild-type test animal The promoter may or may not b the native gene promoter of the transgene.

30   In another embodiment, the invention involves a method for modulating the activity of a polypeptide with an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, the method including introducing a cell

sample expressing the polypeptide with a compound that binds to the polypeptide in an amount sufficient to modulate the activity of the polypeptide.

In another embodiment, the invention involves a method of treating or preventing a pathology associated with a polypeptide with an amino acid sequence selected from the

5   group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, the method including administering the polypeptide to a subject in which such treatment or prevention is desired in an amount sufficient to treat or prevent the pathology in the subject. The subject could be human.

In another embodiment, the invention involves a method of treating a pathological

10   state in a mammal, the method including administering to the mammal a polypeptide in an amount that is sufficient to alleviate the pathological state, wherein the polypeptide is a polypeptide having an amino acid sequence at least 95% identical to a polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, or a biologically active fragment thereof.

15   In another embodiment, the invention involves an isolated nucleic acid molecule comprising a nucleic acid sequence encoding a polypeptide having an amino acid sequence selected from the group consisting of a mature form of the amino acid sequence given SEQ ID NO:2n, wherein n is an integer between 1 and 127; a variant of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an

20   integer between 1 and 127, wherein any amino acid in the mature form of the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed; the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127; a variant of the amino acid sequence selected from the group consisting of SEQ ID

25   NO:2n, wherein n is an integer between 1 and 127, in which any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed; a nucleic acid fragment encoding at least a portion of a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, or any variant of

30   the polypeptide wherein any amino acid of the chosen sequence is changed to a different amino acid, provided that no more than 10% of the amino acid residues in the sequence are so changed; and the complement of any of the nucleic acid molecules.

In another embodiment, the invention comprises an isolated nucleic acid molecule having a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a mature form of the amino acid sequence given SEQ ID NO:2n, wherein n is an integer between 1 and 127, wherein the nucleic acid molecule
5   comprises the nucleotide sequence of a naturally occurring allelic nucleic acid variant.

In another embodiment, the invention involves an isolated nucleic acid molecule including a nucleic acid sequence encoding a polypeptide having an amino acid sequence selected from the group consisting of a mature form of the amino acid sequence given SEQ ID NO:2n, wherein n is an integer between 1 and 127, that encodes a variant polypeptide,
10   wherein the variant polypeptide has the polypeptide sequence of a naturally occurring polypeptide variant.

In another embodiment, the invention comprises an isolated nucleic acid molecule having a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of a mature form of the amino acid sequence given SEQ
15   ID NO:2n, wherein n is an integer between 1 and 127, wherein the nucleic acid molecule differs by a single nucleotide from a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 2n-1, wherein n is an integer between 1 and 127.

In another embodiment, the invention includes an isolated nucleic acid molecule having a nucleic acid sequence encoding a polypeptide including an amino acid sequence
20   selected from the group consisting of a mature form of the amino acid sequence given SEQ ID NO:2n, wherein n is an integer between 1 and 127, wherein the nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of the nucleotide sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127; a nucleotide sequence wherein one or more nucleotides in the
25   nucleotide sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed; a nucleic acid fragment of the sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127; and a nucleic
30   acid fragment wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, is

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changed from that selected from the group consisting of the chosen sequence to a different
nucleotide provided that no more than 15% of the nucleotides are so changed.

In another embodiment, the invention includes an isolated nucleic acid molecule
having a nucleic acid sequence encoding a polypeptide including an amino acid sequence
5   selected from the group consisting of a mature form of the amino acid sequence given SEQ
ID NO:2n, wherein n is an integer between 1 and 127, wherein the nucleic acid molecule
hybridizes under stringent conditions to the nucleotide sequence selected from the group
consisting of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, or a
complement of the nucleotide sequence.

10   In another embodiment, the invention includes an isolated nucleic acid molecule
having a nucleic acid sequence encoding a polypeptide including an amino acid sequence
selected from the group consisting of a mature form of the amino acid sequence given SEQ
ID NO:2n, wherein n is an integer between 1 and 127, wherein the nucleic acid molecule
has a nucleotide sequence in which any nucleotide specified in the coding sequence of the
15   chosen nucleotide sequence is changed from that selected from the group consisting of the
chosen sequence to a different nucleotide provided that no more than 15% of the
nucleotides in the chosen coding sequence are so changed, an isolated second
polynucleotide that is a complement of the first polynucleotide, or a fragment of any of
them.

20   In another embodiment, the invention includes a vector involving the nucleic acid
molecule having a nucleic acid sequence encoding a polypeptide including an amino acid
sequence selected from the group consisting of a mature form of the amino acid sequence
given SEQ ID NO:2n, wherein n is an integer between 1 and 127. This vector can have a
promoter operably linked to the nucleic acid molecule. This vector can be located within a
25   cell.

In another embodiment, the invention involves a method for determining the
presence or amount of a nucleic acid molecule having a nucleic acid sequence encoding a
polypeptide including an amino acid sequence selected from the group consisting of a
mature form of the amino acid sequence given SEQ ID NO:2n, wherein n is an integer
30   between 1 and 127, in a sample, the method including providing the sample; introducing the
sample to a probe that binds to the nucleic acid molecule; and determining the presence or
amount of the probe bound to the nucleic acid molecule, thereby determining the presence

or amount of the nucleic acid molecule in the sample. The presence or amount of the nucleic acid molecule is used as a marker for cell or tissue type. The cell type can be cancerous.

In another embodiment, the invention involves a method for determining the presence of or predisposition for a disease associated with altered levels of a nucleic acid

5   molecule having a nucleic acid sequence encoding a polypeptide including an amino acid sequence selected from the group consisting of a mature form of the amino acid sequence given SEQ ID NO:2n, wherein n is an integer between 1 and 127, in a first mammalian subject, the method including measuring the amount of the nucleic acid in a sample from the first mammalian subject; and comparing the amount of the nucleic acid in the sample of

10   step (a) to the amount of the nucleic acid present in a control sample from a second mammalian subject known not to have or not be predisposed to, the disease; wherein an alteration in the level of the nucleic acid in the first subject as compared to the control sample indicates the presence of or predisposition to the disease.

The invention further provides an antibody that binds immunospecifically to a

15   NOVX polypeptide. The NOVX antibody may be monoclonal, humanized, or a fully human antibody. Preferably, the antibody has a dissociation constant for the binding of the NOVX polypeptide to the antibody less than 1×10^{-9} M. More preferably, the NOVX antibody neutralizes the activity of the NOVX polypeptide.

In a further aspect, the invention provides for the use of a therapeutic in the

20   manufacture of a medicament for treating a syndrome associated with a human disease, associated with a NOVX polypeptide. Preferably the therapeutic is a NOVX antibody.

In yet a further aspect, the invention provides a method of treating or preventing a NOVX-associated disorder, a method of treating a pathological state in a mammal, and a method of treating or preventing a pathology associated with a polypeptide by administering

25   a NOVX antibody to a subject in an amount sufficient to treat or prevent the disorder.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and

30   materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of

conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

5   **BRIEF DESCRIPTION OF THE FIGURES**

Figure 1 is a Western blot showing expression of NOV30b (CG51117-05) immunoreactive polypeptide in human embryonic kidney 293 cells.

Figure 2 is a schematic diagram of the x-ray crystal structure of porcine colipase and tetra ethylene glycol monooctyl ether inhibitor.

10   Figure 3 is a schematic diagram showing the interfacial binding domain of colipase.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel nucleotides and polypeptides encoded thereby. Included in the invention are the novel nucleic acid sequences, their encoded polypeptides, antibodies, and other related compounds. The sequences are collectively referred to herein

15   as "NOVX nucleic acids" or "NOVX polynucleotides" and the corresponding encoded polypeptides are referred to as "NOVX polypeptides" or "NOVX proteins." Unless indicated otherwise, "NOVX" is meant to refer to any of the novel sequences disclosed herein. Table A provides a summary of the NOVX nucleic acids and their encoded polypeptides.

20   TABLE A. Sequences and Corresponding SEQ ID Numbers

NOVX Assignment	Internal Identification	SEQ ID NO (nucleic acid)	SEQ ID NO (amino acid)	Homology
NOV1a	CG108440-01	1	2	Fibronectin precursor protein-like protein
NOV1b	CG108440-02	3	4	Fibronectin precursor protein-like protein
NOV2a	CG122589-01	5	6	Asialoglycoprotein receptor 2-like protein
NOV2b	CG122589-02	7	8	Asialoglycoprotein receptor 2-like protein
NOV2c	CG122589-03	9	10	Asialoglycoprotein receptor 2-like protein

NOV3a	CG133274-01	11	12	Induced myeloid leukemia cell differentiation protein MCL-1-like protein
NOV3b	CG133274-02	13	14	Induced myeloid leukemia cell differentiation protein MCL-1-like protein
NOV3c	278876765	15	16	Induced myeloid leukemia cell differentiation protein MCL-1-like protein
NOV3d	278881214	17	18	Induced myeloid leukemia cell differentiation protein MCL-1-like protein
NOV4a	CG134430-01	19	20	RIKEN cDNA 2310034104-like protein
NOV5a	CG137677-01	21	22	RIKEN 5730409G15-like protein
NOV6a	CG137697-01	23	24	RIKEN 5730409G15-like protein
NOV7a	CG137717-01	25	26	FLJ37712 fis protein-like protein
NOV8a	CG137793-01	27	28	High affinity immunoglobulin epsilon receptor alpha subunit precursor protein-like protein
NOV8b	CG137793-02	29	30	High affinity immunoglobulin epsilon receptor alpha subunit precursor protein-like protein
NOV9a	CG137873-01	31	32	Fibrinogen alpha chain precursor protein-like protein
NOV9b	CG137873-03	33	34	Fibrinogen alpha chain precursor protein-like protein
NOV9c	CG137873-02	35	36	Fibrinogen alpha chain precursor protein-like protein
NOV10a	CG137882-01	37	38	FLJ21269-like protein
NOV10b	CG137882-02	39	40	FLJ21269-like protein
NOV11a	CG137910-01	41	42	FLJ21432-like protein
NOV12a	CG138013-01	43	44	Sialic acid-binding immunoglobulin-like lectin-9-like protein
NOV13a	CG138074-01	45	46	RIKEN 2310012P03-like protein
NOV14a	CG138573-01	47	48	Folate receptor 3-like protein
NOV15a	CG138606-01	49	50	Brush border 61.9 KDa protein precursor-like protein

NOV16a	CG138751-01	51	52	cAMP inducible 2 protein-like protein
NOV16b	CG138751-02	53	54	cAMP inducible 2 protein-like protein
NOV17a	CG139062-01	55	56	Jagged 1 precursor protein-like protein
NOV17b	CG139062-02	57	58	Jagged 1 precursor protein-like protein
NOV18a	CG139363-01	59	60	Transmembrane protein HTMP10-like protein
NOV18b	CG139363-02	61	62	Transmembrane protein HTMP10-like protein
NOV19a	CG140188-01	63	64	DC2-like protein
NOV20a	CG140305-01	65	66	Complement-c1q tumor necrosis factor-related protein-like protein
NOV20b	CG140305-02	67	68	Complement-c1q tumor necrosis factor-related protein-like protein
NOV21a	CG140639-01	69	70	Flotillin-2 (Reggie-1) (REG-1)-like protein
NOV21b	CG140639-02	71	72	Flotillin-2 (Reggie-1) (REG-1)-like protein
NOV22a	CG140843-01	73	74	Integrin beta-5 precursor protein-like protein
NOV23a	CG141540-01	75	76	IL1 receptor-type 2-like protein
NOV23b	CG141540-02	77	78	IL1 receptor-type 2-like protein
NOV24a	CG141580-01	79	80	KIAA 1467 protein-like protein
NOV25a	CG141643-01	81	82	RIKEN 2010001CC9 protein-like protein
NOV26a	CG142003-01	83	84	Plasma protease C1 inhibitor precursor protein-like protein
NOV26b	306076006	85	86	Plasma protease C1 inhibitor precursor protein-like protein
NOV26c	278889088	87	88	Plasma protease C1 inhibitor precursor protein-like protein
NOV26d	CG142003-02	89	90	Plasma protease C1 inhibitor precursor protein-like protein
NOV27a	CG142023-01	91	92	6230421J19Rik protein-like protein
NOV28a	CG142092-01	93	94	C4b-binding protein alpha chain precursor protein-like protein
NOV28b	CG142092-02	95	96	C4b-binding protein alpha chain precursor protein-like protein
NOV28c	CG142092-03	97	98	C4b-binding protein alpha chain precursor protein-like protein

NOV29a	CG171681-01	99	100	Sushi repeat-containing protein
NOV29b	CG171681-03	101	102	Sushi repeat-containing protein
NOV29c	CG171681-02	103	104	Sushi repeat-containing protein
NOV30a	CG51117-01	105	106	Nephronectin-like protein
NOV30b	CG51117-05	107	108	Nephronectin-like protein
NOV30c	CG51117-06	109	110	Nephronectin-like protein
NOV30d	CG51117-07	111	112	Nephronectin-like protein
NOV30e	CG51117-03	113	114	Nephronectin-like protein
NOV30f	CG51117-02	115	116	Nephronectin-like protein
NOV30g	CG51117-04	117	118	Nephronectin-like protein
NOV30h	CG51117-08	119	120	Nephronectin-like protein
NOV30i	CG51117-09	121	122	Nephronectin-like protein
NOV31a	CG51264-01	123	124	ST7-like protein
NOV31b	CG51264-03	125	126	ST7-like protein
NOV31c	CG51264-04	127	128	ST7-like protein
NOV31d	CG51264-06	129	130	ST7-like protein
NOV31e	CG51264-07	131	132	ST7-like protein
NOV31f	CG51264-02	133	134	ST7-like protein
NOV31g	CG51264-05	135	136	ST7-like protein
NOV31h	CG51264-08	137	138	ST7-like protein
NOV31i	CG51264-09	139	140	ST7-like protein
NOV31j	CG51264-10	141	142	ST7-like protein
NOV31k	CG51264-11	143	144	ST7-like protein
NOV31l	CG51264-12	145	146	ST7-like protein
NOV31m	CG51264-13	147	148	ST7-like protein
NOV31n	CG51264-14	149	150	ST7-like protein
NOV31o	CG51264-15	151	152	ST7-like protein
NOV31p	CG51264-16	153	154	ST7-like protein
NOV32a	CG52423-01	155	156	PV-1-like protein
NOV33a	CG52919-01	157	158	Sez-6-like protein
NOV33b	CG52919-02	159	160	Sez-6-like protein
NOV33c	CG52919-03	161	162	Sez-6-like protein
NOV33d	CG52919-04	163	164	Sez-6-like protein
NOV33e	CG52919-05	165	166	Sez-6-like protein
NOV33f	CG52919-06	167	168	Sez-6-like protein
NOV33g	CG52919-01	169	170	Sez-6-like protein
NOV33h	CG52919-07	171	172	Sez-6-like protein
NOV33i	CG52919-08	173	174	Sez-6-like protein
NOV33j	CG52919-09	175	176	Sez-6-like protein
NOV34a	CG55698-01	177	178	Colipase precursor protein-like protein
NOV34b	CG55698-02	179	180	Colipase precursor protein-like protein
NOV35a	CG55832-01	181	182	Tenascin-C precursor protein-like protein

NOV35b	CG55832-03	183	184	Tenascin-C precursor protein-like protein
NOV35c	CG55832-02	185	186	Tenascin-C precursor protein-like protein
NOV36a	CG56054-01	187	188	Integrin alpha 7-like protein
NOV36b	CG56054-03	189	190	Integrin alpha 7-like protein
NOV36c	CG56054-04	191	192	Integrin alpha 7-like protein
NOV36d	CG56054-05	193	194	Integrin alpha 7-like protein
NOV36e	CG56054-06	195	196	Integrin alpha 7-like protein
NOV36f	CG56054-07	197	198	Integrin alpha 7-like protein
NOV36g	CG56054-08	199	200	Integrin alpha 7-like protein
NOV36h	CG56054-09	201	202	Integrin alpha 7-like protein
NOV36i	CG56054-10	203	204	Integrin alpha 7-like protein
NOV36j	CG56054-11	205	206	Integrin alpha 7-like protein
NOV36k	CG56054-12	207	208	Integrin alpha 7-like protein
NOV36l	CG56054-13	209	210	Integrin alpha 7-like protein
NOV36m	CG56054-14	211	212	Integrin alpha 7-like protein
NOV36n	CG56054-15	213	214	Integrin alpha 7-like protein
NOV36o	CG56054-16	215	216	Integrin alpha 7-like protein
NOV36p	CG56054-17	217	218	Integrin alpha 7-like protein
NOV36q	CG56054-18	219	220	Integrin alpha 7-like protein
NOV36r	CG56054-19	221	222	Integrin alpha 7-like protein
NOV36s	CG56054-02	223	224	Integrin alpha 7-like protein
NOV37a	CG88634-01	225	226	KIAA1219-like protein
NOV38a	CG97012-01	227	228	Seizure 6 precursor protein-like protein
NOV38b	CG97012-02	229	230	Seizure 6 precursor protein-like protein
NOV38c	CG97012-03	231	232	Seizure 6 precursor protein-like protein
NOV38d	CG97012-01	233	234	Seizure 6 precursor protein-like protein
NOV38e	210120300	235	236	Seizure 6 precursor protein-like protein
NOV38f	210120376	237	238	Seizure 6 precursor protein-like protein
NOV38g	210120463	239	240	Seizure 6 precursor protein-like protein
NOV38h	210120269	241	242	Seizure 6 precursor protein-like protein
NOV38i	CG97012-04	243	244	Seizure 6 precursor protein-like protein
NOV38j	CG97012-05	245	246	Seizure 6 precursor protein-like protein
NOV39a	CG99754-01	247	248	RIKEN protein-like protein
NOV39b	CG99754-02	249	250	RIKEN protein-like protein
NOV40a	CG99777-01	251	252	CD30 ligand-like protein
NOV40b	CG99777-02	253	254	CD30 ligand-like protein

Table A indicates the homology of NOVX polypeptides to known protein families. Thus, the nucleic acids and polypeptides, antibodies and related compounds according to the invention corresponding to a NOVX as identified in column 1 of Table A will be useful

5   in therapeutic and diagnostic applications implicated in, for example, pathologies and disorders associated with the known protein families identified in column 5 of Table A.

Pathologies, diseases, disorders, conditions, and the like that are associated with NOVX sequences include, but are not limited to: e.g., cardiomyopathy, atherosclerosis, hypertension, congenital heart defects, aortic stenosis, atrial septal defect (ASD),

10   atrioventricular (A-V) canal defect, ductus arteriosus, pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD), valve diseases, tuberous sclerosis, scleroderma, obesity, metabolic disturbances associated with obesity, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm, hemophilia, hypercoagulation, idiopathic thrombocytopenic purpura, immunodeficiencies, graft versus

15   host disease, AIDS, bronchial asthma, Crohn's disease; multiple sclerosis, treatment of Albright Hereditary Ostoeodystrophy, infectious disease, anorexia, cancer-associated cachexia, , neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disease, immune disorders, hematopoietic disorders, and the various dyslipidemias, the metabolic syndrome X, wasting disorders associated with chronic diseases, cancer, e.g., uterine cancer,

20   lymphoma, adenocarcinoma, as well as conditions such as transplantation, neuroprotection, fertility, or regeneration (in vitro and in vivo).

NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence

25   of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the family to which the NOVX polypeptides belong.

Consistent with other known members of the family of proteins, identified in column 5 of Table A, the NOVX polypeptides of the present invention show homology to,

30   and contain domains that are characteristic of, other members of such protein families. Details of the sequence relatedness and domain analysis for each NOVX are presented in Example A.

The NOVX nucleic acids and polypeptides can also be used to screen for molecules, which inhibit or enhance NOVX activity or function. Specifically, the nucleic acids and polypeptides according to the invention may be used as targets for the identification of small molecules that modulate or inhibit diseases associated with the protein families listed
5   in Table A.

The NOVX nucleic acids and polypeptides are also useful for detecting specific cell types. Details of the expression analysis for each NOVX are presented in Example C. Accordingly, the NOVX nucleic acids, polypeptides, antibodies and related compounds according to the invention will have diagnostic and therapeutic applications in the detection
10   of a variety of diseases with differential expression in normal vs. diseased tissues, *e.g.* detection of a variety of cancers.

Additional utilities for NOVX nucleic acids and polypeptides according to the invention are disclosed herein.

NOVX clones

15   NOVX nucleic acids and their encoded polypeptides are useful in a variety of applications and contexts. The various NOVX nucleic acids and polypeptides according to the invention are useful as novel members of the protein families according to the presence of domains and sequence relatedness to previously described proteins. Additionally, NOVX nucleic acids and polypeptides can also be used to identify proteins that are members of the
20   family to which the NOVX polypeptides belong.

The NOVX genes and their corresponding encoded proteins are useful for preventing, treating or ameliorating medical conditions, *e.g.*, by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are
25   described for each of the NOVX genes, based on the tissues in which they are most highly expressed. Uses include developing products for the diagnosis or treatment of a variety of diseases and disorders.

The NOVX nucleic acids and proteins of the invention are useful in potential diagnostic and therapeutic applications and as a research tool. These include serving as a
30   specific or selective nucleic acid or protein diagnostic and/or prognostic marker, wherein the presence or amount of the nucleic acid or the protein are to be assessed, as well as

potential therapeutic applications such as the following: (i) a protein therapeutic, (ii) a small molecule drug target, (iii) an antibody target (therapeutic, diagnostic, drug targeting/cytotoxic antibody), (iv) a nucleic acid useful in gene therapy (gene delivery/gene ablation), and (v) a composition promoting tissue regeneration *in vitro* and *in vivo* (vi) a

5   biological defense weapon.

In one specific embodiment, the invention includes an isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 127; (b) a variant of a mature form of the amino acid sequence

10   selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 127, wherein any amino acid in the mature form is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed; (c) an amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 127; (d) a variant of the amino acid

15   sequence selected from the group consisting of SEQ ID NO:2n, wherein n is an integer between 1 and 127, wherein any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed; and (e) a fragment of any of (a) through (d).

In another specific embodiment, the invention includes an isolated nucleic acid

20   molecule comprising a nucleic acid sequence encoding a polypeptide comprising an amino acid sequence selected from the group consisting of: (a) a mature form of the amino acid sequence given SEQ ID NO: 2n, wherein n is an integer between 1 and 127; (b) a variant of a mature form of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 127, wherein any amino acid in the mature

25   form of the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence of the mature form are so changed; (c) the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 127; (d) a variant of the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 127, in which

30   any amino acid specified in the chosen sequence is changed to a different amino acid, provided that no more than 15% of the amino acid residues in the sequence are so changed; (e) a nucleic acid fragment encoding at least a portion of a polypeptide comprising the

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amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is an integer between 1 and 127, or any variant of said polypeptide wherein any amino acid of the chosen sequence is changed to a different amino acid, provided that no more than 10% of the amino acid residues in the sequence are so changed; and (f) the complement of any of

5   said nucleic acid molecules.

In yet another specific embodiment, the invention includes an isolated nucleic acid molecule, wherein said nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 127; (b) a

10   nucleotide sequence wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 127 is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed; (c) a nucleic acid fragment of the sequence selected from the group consisting of SEQ ID NO:

15   2n-1, wherein n is an integer between 1 and 127; and (d) a nucleic acid fragment wherein one or more nucleotides in the nucleotide sequence selected from the group consisting of SEQ ID NO: 2n-1, wherein n is an integer between 1 and 127, is changed from that selected from the group consisting of the chosen sequence to a different nucleotide provided that no more than 15% of the nucleotides are so changed.

20   **NOVX Nucleic Acids and Polypeptides**

One aspect of the invention pertains to isolated nucleic acid molecules that encode NOVX polypeptides or biologically active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify NOVX-encoding nucleic acids (*e.g.*, NOVX mRNAs) and fragments for use as PCR

25   primers for the amplification and/or mutation of NOVX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule may be single-stranded or double-stranded, but preferably is comprised

30   double-stranded DNA.

19

A NOVX nucleic acid can encode a mature NOVX polypeptide. As used herein, a
"mature" form of a polypeptide or protein disclosed in the present invention is the product
of a naturally occurring polypeptide or precursor form or proprotein. The naturally
occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the
5   full-length gene product encoded by the corresponding gene. Alternatively, it may be
defined as the polypeptide, precursor or proprotein encoded by an ORF described herein.
The product "mature" form arises, by way of nonlimiting example, as a result of one or
more naturally occurring processing steps that may take place within the cell (e.g., host cell)
in which the gene product arises. Examples of such processing steps leading to a "mature"
10   form of a polypeptide or protein include the cleavage of the N-terminal methionine residue
encoded by the initiation codon of an ORF, or the proteolytic cleavage of a signal peptide or
leader sequence. Thus a mature form arising from a precursor polypeptide or protein that
has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2
through N remaining after removal of the N-terminal methionine. Alternatively, a mature
15   form arising from a precursor polypeptide or protein having residues 1 to N, in which an
N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues
from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a
polypeptide or protein may arise from a step of post-translational modification other than a
proteolytic cleavage event. Such additional processes include, by way of non-limiting
20   example, glycosylation, myristylation or phosphorylation. In general, a mature polypeptide
or protein may result from the operation of only one of these processes, or a combination of
any of them.

The term "probe", as utilized herein, refers to nucleic acid sequences of variable
length, preferably between at least about 10 nucleotides (nt), about 100 nt, or as many as
25   approximately, e.g., 6,000 nt, depending upon the specific use. Probes are used in the
detection of identical, similar, or complementary nucleic acid sequences. Longer length
probes are generally obtained from a natural or recombinant source, are highly specific, and
much slower to hybridize than shorter-length oligomer probes. Probes may be single-
stranded or double-stranded and designed to have specificity in PCR, membrane-based
30   hybridization technologies, or ELISA-like technologies.

The term "isolated" nucleic acid molecule, as used herein, is a nucleic acid that is
separated from other nucleic acid molecules which are present in the natural source of the

nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated NOVX nucleic acid molecules can contain less than

5   about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb, or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, *etc.*). Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium, or of chemical precursors or other chemicals.

10   A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, or a complement of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, as a

15   hybridization probe, NOVX molecules can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook, *et al.*, (eds.), MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

20   A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template with appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to NOVX nucleotide sequences can be

25   prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides

30   comprise a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at

least 6 contiguous nucleotides of SEQ ID NO:2n-1, wherein n is an integer between 1 and
127, or a complement thereof. Oligonucleotides may be chemically synthesized and may
also be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises
5   a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID
NO:2n-1, wherein n is an integer between 1 and 127, or a portion of this nucleotide
sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a
biologically-active portion of a NOVX polypeptide). A nucleic acid molecule that is
complementary to the nucleotide sequence of SEQ ID NO:2n-1, wherein n is an integer
10 between 1 and 127, is one that is sufficiently complementary to the nucleotide sequence of
SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, that it can hydrogen bond
with few or no mismatches to the nucleotide sequence shown in SEQ ID NO:2n-1, wherein
n is an integer between 1 and 127, thereby forming a stable duplex.

As used herein, the term "complementary" refers to Watson-Crick or Hoogsteen
15 base pairing between nucleotides units of a nucleic acid molecule, and the term "binding"
means the physical or chemical interaction between two polypeptides or compounds or
associated polypeptides or compounds or combinations thereof. Binding includes ionic,
non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can
be either direct or indirect. Indirect interactions may be through or due to the effects of
20 another polypeptide or compound. Direct binding refers to interactions that do not take
place through, or due to, the effect of another polypeptide or compound, but instead are
without other substantial chemical intermediates.

A "fragment" provided herein is defined as a sequence of at least 6 (contiguous)
nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific
25 hybridization in the case of nucleic acids or for specific recognition of an epitope in the case
of amino acids, and is at most some portion less than a full length sequence. Fragments
may be derived from any contiguous portion of a nucleic acid or amino acid sequence of
choice.

A full-length NOVX clone is identified as containing an ATG translation start codon
30 and an in-frame stop codon. Any disclosed NOVX nucleotide sequence lacking an ATG
start codon therefore encodes a truncated C-terminal fragment of the respective NOVX
polypeptide, and requires that the corresponding full-length cDNA extend in the 5' direction

of the disclosed sequence. Any disclosed NOVX nucleotide sequence lacking an in-frame stop codon similarly encodes a truncated N-terminal fragment of the respective NOVX polypeptide, and requires that the corresponding full-length cDNA extend in the 3' direction of the disclosed sequence.

5   A "derivative" is a nucleic acid sequence or amino acid sequence formed from the native compounds either directly, by modification or partial substitution. An "analog" is a nucleic acid sequence or amino acid sequence that has a structure similar to, but not identical to, the native compound, e.g. they differs from it in respect to certain components or side chains. Analogs may be synthetic or derived from a different evolutionary origin

10   and may have a similar or opposite metabolic activity compared to wild type. A "homolog" is a nucleic acid sequence or amino acid sequence of a particular gene that is derived from different species.

         Derivatives and analogs may be full length or other than full length. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to,

15   molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of

20   hybridizing to the complement of a sequence encoding the proteins under stringent, moderately stringent, or low stringent conditions. *See e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below.

         A "homologous nucleic acid sequence" or "homologous amino acid sequence," or

25   variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences include those sequences coding for isoforms of NOVX polypeptides. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the invention,

30   homologous nucleotide sequences include nucleotide sequences encoding for a NOVX polypeptide of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat cow, horse, and other organisms.

Homologous nucleotide sequences also include, but are not limited to, naturally occurring
allelic variations and mutations of the nucleotide sequences set forth herein. A homologous
nucleotide sequence does not, however, include the exact nucleotide sequence encoding
human NOVX protein. Homologous nucleic acid sequences include those nucleic acid

5   sequences that encode conservative amino acid substitutions (see below) in SEQ ID
NO:2n-1, wherein n is an integer between 1 and 127, as well as a polypeptide possessing
NOVX biological activity. Various biological activities of the NOVX proteins are
described below.

A NOVX polypeptide is encoded by the open reading frame ("ORF") of a NOVX

10   nucleic acid. An ORF corresponds to a nucleotide sequence that could potentially be
translated into a polypeptide. A stretch of nucleic acids comprising an ORF is uninterrupted
by a stop codon. An ORF that represents the coding sequence for a full protein begins with
an ATG "start" codon and terminates with one of the three "stop" codons, namely, TAA,
TAG, or TGA. For the purposes of this invention, an ORF may be any part of a coding

15   sequence, with or without a start codon, a stop codon, or both. For an ORF to be considered
as a good candidate for coding for a *bona fide* cellular protein, a minimum size requirement
is often set, *e.g.*, a stretch of DNA that would encode a protein of 50 amino acids or more.

The nucleotide sequences determined from the cloning of the human NOVX genes
allows for the generation of probes and primers designed for use in identifying and/or

20   cloning NOVX homologs in other cell types, *e.g.* from other tissues, as well as NOVX
homologs from other vertebrates. The probe/primer typically comprises substantially
purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide
sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150,
200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence of SEQ ID

25   NO:2n-1, wherein n is an integer between 1 and 127; or an anti-sense strand nucleotide
sequence of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127; or of a naturally
occurring mutant of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127.

Probes based on the human NOVX nucleotide sequences can be used to detect
transcripts or genomic sequences encoding the same or homologous proteins. In various

30   embodiments, the probe has a detectable label attached, *e.g.* the label can be a radioisotope,
a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a
part of a diagnostic test kit for identifying cells or tissues which mis-express a NOVX

protein, such as by measuring a level of a NOVX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting NOVX mRNA levels or determining whether a genomic NOVX gene has been mutated or deleted.

"A polypeptide having a biologically-active portion of a NOVX polypeptide" refers
5   to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically-active portion of NOVX" can be prepared by isolating a portion of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, that encodes a polypeptide having a
10   NOVX biological activity (the biological activities of the NOVX proteins are described below), expressing the encoded portion of NOVX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of NOVX.

NOVX Nucleic Acid and Polypeptide Variants

The invention further encompasses nucleic acid molecules that differ from the
15   nucleotide sequences of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, due to degeneracy of the genetic code and thus encode the same NOVX proteins as that encoded by the nucleotide sequences of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence of SEQ ID NO:$2n$,
20   wherein n is an integer between 1 and 127.

In addition to the human NOVX nucleotide sequences of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of the NOVX polypeptides may exist within a population (*e.g.*, the human population). Such genetic
25   polymorphism in the NOVX genes may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding a NOVX protein, preferably a vertebrate NOVX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the NOVX genes. Any and all such nucleotide
30   variations and resulting amino acid polymorphisms in the NOVX polypeptides, which are

the result of natural allelic variation and that do not alter the functional activity of the NOVX polypeptides, are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding NOVX proteins from other species, and thus that have a nucleotide sequence that differs from a human SEQ ID NO:2n-1, wherein n

5　　is an integer between 1 and 127, are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologs of the NOVX cDNAs of the invention can be isolated based on their homology to the human NOVX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent

10　　hybridization conditions.

Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127. In another embodiment, the nucleic acid is at least 10, 25,

15　　50, 100, 250, 500, 750, 1000, 1500, or 2000 or more nucleotides in length. In yet another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least about 65% homologous to each other typically remain hybridized to each other.

20　　Homologs (i.e., nucleic acids encoding NOVX proteins derived from species other than human) or other related sequences (e.g., paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions

25　　under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5 °C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and

30　　pH. The Tm is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at

excess, at Tm, 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30 °C for short probes, primers or oligonucleotides (e.g., 10 nt

5   to 50 nt) and at least about 60 °C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in Ausubel, et al., (eds.), CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons,

10   N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions are hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm

15   DNA at 65°C, followed by one or more washes in 0.2X SSC, 0.01% BSA at 50 °C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of SEQ ID NO:$2n-1$, wherein n is an integer between 1 and 127, corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs

20   in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:$2n-1$, wherein n is an integer between 1 and 127, or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency

25   hybridization conditions are hybridization in 6X SSC, 5X Reinhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55 °C, followed by one or more washes in 1X SSC, 0.1% SDS at 37 °C. Other conditions of moderate stringency that may be used are well-known within the art. See, e.g., Ausubel, et al. (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Krieger, 1990; GENE TRANSFER AND

30   EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequences of SEQ ID NO:$2n-1$, wherein n is an integer

between 1 and 127, or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10%

5   (wt/vol) dextran sulfate at 40 °C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50 °C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). *See, e.g.*, Ausubel, *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND

10   EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981. *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative Mutations

In addition to naturally-occurring allelic variants of NOVX sequences that may exist in the population, the skilled artisan will further appreciate that changes can be introduced

15   by mutation into the nucleotide sequences of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, thereby leading to changes in the amino acid sequences of the encoded NOVX protein, without altering the functional ability of that NOVX protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of SEQ ID NO:$2n$, wherein n is an integer between 1

20   and 127. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the NOVX proteins without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the NOVX proteins of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which

25   conservative substitutions can be made are well-known within the art.

Another aspect of the invention pertains to nucleic acid molecules encoding NOVX proteins that contain changes in amino acid residues that are not essential for activity. Such NOVX proteins differ in amino acid sequence from SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, yet retain biological activity. In one embodiment, the isolated

30   nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 40% homologous to the amino acid sequences of SEQ ID NO:$2n$, wherein n is an integer between 1 and 127. Preferably, the

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protein encoded by the nucleic acid molecule is at least about 60% homologous to SEQ ID NO:2n, wherein n is an integer between 1 and 127; more preferably at least about 70% homologous to SEQ ID NO:2n, wherein n is an integer between 1 and 127; still more preferably at least about 80% homologous to SEQ ID NO:2n, wherein n is an integer

5   between 1 and 127; even more preferably at least about 90% homologous to SEQ ID NO:2n, wherein n is an integer between 1 and 127; and most preferably at least about 95% homologous to SEQ ID NO:2n, wherein n is an integer between 1 and 127.

An isolated nucleic acid molecule encoding a NOVX protein homologous to the protein of SEQ ID NO:2n, wherein n is an integer between 1 and 127, can be created by

10   introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced any one of SEQ ID NO:2n-1, wherein n is an integer

15   between 1 and 127, by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted, non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have

20   been defined within the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and

25   aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted non-essential amino acid residue in the NOVX protein is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a NOVX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for NOVX biological

30   activity to identify mutants that retain activity. Following mutagenesis of a nucleic acid of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, the encoded protein can be

expressed by any recombinant technology known in the art and the activity of the protein can be determined.

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved "strong" residues or fully

5   conserved "weak" residues. The "strong" group of conserved amino acid residues may be any one of the following groups: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the "weak" group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK, STPA, SGND, SNDEQK, NDEQHK,

10   NEQHRK, HFY, wherein the letters within each group represent the single letter amino acid code.

In one embodiment, a mutant NOVX protein can be assayed for (*i*) the ability to form protein:protein interactions with other NOVX proteins, other cell-surface proteins, or biologically-active portions thereof, (*ii*) complex formation between a mutant NOVX

15   protein and a NOVX ligand; or (*iii*) the ability of a mutant NOVX protein to bind to an intracellular target protein or biologically-active portion thereof; (*e.g.* avidin proteins).

In yet another embodiment, a mutant NOVX protein can be assayed for the ability to regulate a specific biological function (*e.g.*, regulation of insulin release).

Interfering RNA

20   In one aspect of the invention, NOVX gene expression can be attenuated by RNA interference. One approach well-known in the art is short interfering RNA (siRNA) mediated gene silencing where expression products of a NOVX gene are targeted by specific double stranded NOVX derived siRNA nucleotide sequences that are complementary to at least a 19-25 nt long segment of the NOVX gene transcript, including

25   the 5' untranslated (UT) region, the ORF, or the 3' UT region. *See, e.g.*, PCT applications WO00/44895, WO99/32619, WO01/75164, WO01/92513, WO 01/29058, WO01/89304, WO02/16620, and WO02/29858, each incorporated by reference herein in their entirety. Targeted genes can be a NOVX gene, or an upstream or downstream modulator of the NOVX gene. Nonlimiting examples of upstream or downstream modulators of a NOVX

30   gene include, *e.g.*, a transcription factor that binds the NOVX gene promoter, a kinase or

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phosphatase that interacts with a NOVX polypeptide, and polypeptides involved in a NOVX regulatory pathway.

According to the methods of the present invention, NOVX gene expression is silenced using short interfering RNA. A NOVX polynucleotide according to the invention

5   includes a siRNA polynucleotide. Such a NOVX siRNA can be obtained using a NOVX polynucleotide sequence, for example, by processing the NOVX ribopolynucleotide sequence in a cell-free system, such as but not limited to a Drosophila extract, or by transcription of recombinant double stranded NOVX RNA or by chemical synthesis of nucleotide sequences homologous to a NOVX sequence. *See, e.g.*, Tuschl, Zamore,

10   Lehmann, Bartel and Sharp (1999), Genes & Dev. 13: 3191-3197, incorporated herein by reference in its entirety. When synthesized, a typical 0.2 micromolar-scale RNA synthesis provides about 1 milligram of siRNA, which is sufficient for 1000 transfection experiments using a 24-well tissue culture plate format.

The most efficient silencing is generally observed with siRNA duplexes composed

15   of a 21-nt sense strand and a 21-nt antisense strand, paired in a manner to have a 2-nt 3' overhang. The sequence of the 2-nt 3' overhang makes an additional small contribution to the specificity of siRNA target recognition. The contribution to specificity is localized to the unpaired nucleotide adjacent to the first paired bases. In one embodiment, the nucleotides in the 3' overhang are ribonucleotides. In an alternative embodiment, the nucleotides in the

20   3' overhang are deoxyribonucleotides. Using 2'-deoxyribonucleotides in the 3' overhangs is as efficient as using ribonucleotides, but deoxyribonucleotides are often cheaper to synthesize and are most likely more nuclease resistant.

A contemplated recombinant expression vector of the invention comprises a NOVX DNA molecule cloned into an expression vector comprising operatively-linked regulatory

25   sequences flanking the NOVX sequence in a manner that allows for expression (by transcription of the DNA molecule) of both strands. An RNA molecule that is antisense to NOVX mRNA is transcribed by a first promoter (*e.g.*, a promoter sequence 3' of the cloned DNA) and an RNA molecule that is the sense strand for the NOVX mRNA is transcribed by a second promoter (*e.g.*, a promoter sequence 5' of the cloned DNA). The sense and

30   antisense strands may hybridize in vivo to generate siRNA constructs for silencing of the NOVX gene. Alternatively, two constructs can be utilized to create the sense and anti-sense strands of a siRNA construct. Finally, cloned DNA can encode a construct having secondary structure, wherein a single transcript has both the sense and complementary

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antisense sequences from the target gene or genes. In an example of this embodiment, a hairpin RNAi product is homologous to all or a portion of the target gene. In another example, a hairpin RNAi product is a siRNA. The regulatory sequences flanking the NOVX sequence may be identical or may be different, such that their expression may be

5   modulated independently, or in a temporal or spatial manner.

In a specific embodiment, siRNAs are transcribed intracellularly by cloning the NOVX gene templates into a vector containing, e.g., a RNA pol III transcription unit from the smaller nuclear RNA (snRNA) U6 or the human RNase P RNA H1. One example of a vector system is the GeneSuppressor™ RNA Interference kit (commercially available from

10   Imgenex). The U6 and H1 promoters are members of the type III class of Pol III promoters. The +1 nucleotide of the U6-like promoters is always guanosine, whereas the +1 for H1 promoters is adenosine. The termination signal for these promoters is defined by five consecutive thymidines. The transcript is typically cleaved after the second uridine. Cleavage at this position generates a 3' UU overhang in the expressed siRNA, which is

15   similar to the 3' overhangs of synthetic siRNAs. Any sequence less than 400 nucleotides in length can be transcribed by these promoter, therefore they are ideally suited for the expression of around 21-nucleotide siRNAs in, e.g., an approximately 50-nucleotide RNA stem-loop transcript.

A siRNA vector appears to have an advantage over synthetic siRNAs where long

20   term knock-down of expression is desired. Cells transfected with a siRNA expression vector would experience steady, long-term mRNA inhibition. In contrast, cells transfected with exogenous synthetic siRNAs typically recover from mRNA suppression within seven days or ten rounds of cell division. The long-term gene silencing ability of siRNA expression vectors may provide for applications in gene therapy.

25   In general, siRNAs are chopped from longer dsRNA by an ATP-dependent ribonuclease called DICER. DICER is a member of the RNase III family of double-stranded RNA-specific endonucleases. The siRNAs assemble with cellular proteins into an endonuclease complex. *In vitro* studies in Drosophila suggest that the siRNAs/protein complex (siRNP) is then transferred to a second enzyme complex, called an RNA-induced

30   silencing complex (RISC), which contains an endoribonuclease that is distinct from DICER. RISC uses the sequence encoded by the antisense siRNA strand to find and destroy mRNAs of complementary sequence. The siRNA thus acts as a guide, restricting the ribonuclease to cleave only mRNAs complementary to one of the two siRNA strands.

A NOVX mRNA region to be targeted by siRNA is generally selected from a desired NOVX sequence beginning 50 to 100 nt downstream of the start codon. Alternatively, 5' or 3' UTRs and regions nearby the start codon can be used but are generally avoided, as these may be richer in regulatory protein binding sites. UTR-binding proteins and/or translation initiation complexes may interfere with binding of the siRNP or RISC endonuclease complex. An initial BLAST homology search for the selected siRNA sequence is done against an available nucleotide sequence library to ensure that only one gene is targeted. Specificity of target recognition by siRNA duplexes indicate that a single point mutation located in the paired region of an siRNA duplex is sufficient to abolish target mRNA degradation. See, Elbashir *et al.* 2001 EMBO J. 20(23):6877-88. Hence, consideration should be taken to accommodate SNPs, polymorphisms, allelic variants or species-specific variations when targeting a desired gene.

In one embodiment, a complete NOVX siRNA experiment includes the proper negative control. A negative control siRNA generally has the same nucleotide composition as the NOVX siRNA but lack significant sequence homology to the genome. Typically, one would scramble the nucleotide sequence of the NOVX siRNA and do a homology search to make sure it lacks homology to any other gene.

Two independent NOVX siRNA duplexes can be used to knock-down a target NOVX gene. This helps to control for specificity of the silencing effect. In addition, expression of two independent genes can be simultaneously knocked down by using equal concentrations of different NOVX siRNA duplexes, *e.g.*, a NOVX siRNA and an siRNA for a regulator of a NOVX gene or polypeptide. Availability of siRNA-associating proteins is believed to be more limiting than target mRNA accessibility.

A targeted NOVX region is typically a sequence of two adenines (AA) and two thymidines (TT) divided by a spacer region of nineteen (N19) residues (*e.g.*, AA(N19)TT). A desirable spacer region has a G/C-content of approximately 30% to 70%, and more preferably of about 50%. If the sequence AA(N19)TT is not present in the target sequence, an alternative target region would be AA(N21). The sequence of the NOVX sense siRNA corresponds to (N19)TT or N21, respectively. In the latter case, conversion of the 3' end of the sense siRNA to TT can be performed if such a sequence does not naturally occur in the NOVX polynucleotide. The rationale for this sequence conversion is to generate a symmetric duplex with respect to the sequence composition of the sense and antisense 3' overhangs. Symmetric 3' overhangs may help to ensure that the siRNPs are formed with

approximately equal ratios of sense and antisense target RNA-cleaving siRNPs. *See, e.g.,*
Elbashir, Lendeckel and Tuschl (2001). Genes & Dev. 15: 188-200, incorporated by
reference herein in its entirely. The modification of the overhang of the sense sequence of
the siRNA duplex is not expected to affect targeted mRNA recognition, as the antisense
5   siRNA strand guides target recognition.

Alternatively, if the NOVX target mRNA does not contain a suitable AA(N21)
sequence, one may search for the sequence NA(N21). Further, the sequence of the sense
strand and antisense strand may still be synthesized as 5' (N19)TT, as it is believed that the
sequence of the 3'-most nucleotide of the antisense siRNA does not contribute to specificity.
10   Unlike antisense or ribozyme technology, the secondary structure of the target mRNA does
not appear to have a strong effect on silencing. *See,* Harborth, *et al.* (2001) J. Cell Science
114: 4557-4565, incorporated by reference in its entirety.

Transfection of NOVX siRNA duplexes can be achieved using standard nucleic acid
transfection methods, for example, OLIGOFECTAMINE Reagent (commercially available
15   from Invitrogen). An assay for NOVX gene silencing is generally performed approximately
2 days after transfection. No NOVX gene silencing has been observed in the absence of
transfection reagent, allowing for a comparative analysis of the wild-type and silenced
NOVX phenotypes. In a specific embodiment, for one well of a 24-well plate,
approximately 0.84 μg of the siRNA duplex is generally sufficient. Cells are typically
20   seeded the previous day, and are transfected at about 50% confluence. The choice of cell
culture media and conditions are routine to those of skill in the art, and will vary with the
choice of cell type. The efficiency of transfection may depend on the cell type, but also on
the passage number and the confluency of the cells. The time and the manner of formation
of siRNA-liposome complexes (*e.g.* inversion versus vortexing) are also critical. Low
25   transfection efficiencies are the most frequent cause of unsuccessful NOVX silencing. The
efficiency of transfection needs to be carefully examined for each new cell line to be used.
Preferred cell are derived from a mammal, more preferably from a rodent such as a rat or
mouse, and most preferably from a human. Where used for therapeutic treatment, the cells
are preferentially autologous, although non-autologous cell sources are also contemplated as
30   within the scope of the present invention.

For a control experiment, transfection of 0.84 μg single-stranded sense NOVX
siRNA will have no effect on NOVX silencing, and 0.84 μg antisense siRNA has a weak
silencing effect when compared to 0.84 μg of duplex siRNAs. Control experiments again

allow for a comparative analysis of the wild-type and silenced NOVX phenotypes. To control for transfection efficiency, targeting of common proteins is typically performed, for example targeting of lamin A/C or transfection of a CMV-driven EGFP-expression plasmid (*e.g.* commercially available from Clontech). In the above example, a determination of the

5   fraction of lamin A/C knockdown in cells is determined the next day by such techniques as immunofluorescence, Western blot, Northern blot or other similar assays for protein expression or gene expression. Lamin A/C monoclonal antibodies may be obtained from Santa Cruz Biotechnology.

Depending on the abundance and the half life (or turnover) of the targeted NOVX

10   polynucleotide in a cell, a knock-down phenotype may become apparent after 1 to 3 days, or even later. In cases where no NOVX knock-down phenotype is observed, depletion of the NOVX polynucleotide may be observed by immunofluorescence or Western blotting. If the NOVX polynucleotide is still abundant after 3 days, cells need to be split and transferred to a fresh 24-well plate for re-transfection. If no knock-down of the targeted protein is

15   observed, it may be desirable to analyze whether the target mRNA (NOVX or a NOVX upstream or downstream gene) was effectively destroyed by the transfected siRNA duplex. Two days after transfection, total RNA is prepared, reverse transcribed using a target-specific primer, and PCR-amplified with a primer pair covering at least one exon-exon junction in order to control for amplification of pre-mRNAs. RT/PCR of a non-targeted

20   mRNA is also needed as control. Effective depletion of the mRNA yet undetectable reduction of target protein may indicate that a large reservoir of stable NOVX protein may exist in the cell. Multiple transfection in sufficiently long intervals may be necessary until the target protein is finally depleted to a point where a phenotype may become apparent. If multiple transfection steps are required, cells are split 2 to 3 days after transfection. The

25   cells may be transfected immediately after splitting.

An inventive therapeutic method of the invention contemplates administering a NOVX siRNA construct as therapy to compensate for increased or aberrant NOVX expression or activity. The NOVX ribopolynucleotide is obtained and processed into siRNA fragments, or a NOVX siRNA is synthesized, as described above. The NOVX

30   siRNA is administered to cells or tissues using known nucleic acid transfection techniques, as described above. A NOVX siRNA specific for a NOVX gene will decrease or knockdown NOVX transcription products, which will lead to reduced NOVX polypeptide production, resulting in reduced NOVX polypeptide activity in the cells or tissues.

The present invention also encompasses a method of treating a disease or condition associated with the presence of a NOVX protein in an individual comprising administering to the individual an RNAi construct that targets the mRNA of the protein (the mRNA that encodes the protein) for degradation. A specific RNAi construct includes a siRNA or a

5   double stranded gene transcript that is processed into siRNAs. Upon treatment, the target protein is not produced or is not produced to the extent it would be in the absence of the treatment.

Where the NOVX gene function is not correlated with a known phenotype, a control sample of cells or tissues from healthy individuals provides a reference standard for

10   determining NOVX expression levels. Expression levels are detected using the assays described, e.g., RT-PCR, Northern blotting, Western blotting, ELISA, and the like. A subject sample of cells or tissues is taken from a mammal, preferably a human subject, suffering from a disease state. The NOVX ribopolynucleotide is used to produce siRNA constructs, that are specific for the NOVX gene product. These cells or tissues are treated

15   by administering NOVX siRNA's to the cells or tissues by methods described for the transfection of nucleic acids into a cell or tissue, and a change in NOVX polypeptide or polynucleotide expression is observed in the subject sample relative to the control sample, using the assays described. This NOVX gene knockdown approach provides a rapid method for determination of a NOVX minus (NOVX⁻) phenotype in the treated subject

20   sample. The NOVX⁻ phenotype observed in the treated subject sample thus serves as a marker for monitoring the course of a disease state during treatment.

In specific embodiments, a NOVX siRNA is used in therapy. Methods for the generation and use of a NOVX siRNA are known to those skilled in the art. Example techniques are provided below.

25   **Production of RNAs**

Sense RNA (ssRNA) and antisense RNA (asRNA) of NOVX are produced using known methods such as transcription in RNA expression vectors. In the initial experiments, the sense and antisense RNA are about 500 bases in length each. The produced ssRNA and asRNA (0.5 µM) in 10 mM Tris-HCl (pH 7.5) with 20 mM NaCl were heated to 95° C for 1

30   min then cooled and annealed at room temperature for 12 to 16 h. The RNAs are precipitated and resuspended in lysis buffer (below). To monitor annealing, RNAs are electrophoresed in a 2% agarose gel in TBE buffer and stained with ethidium bromide. See,

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e.g., Sambrook *et al.*, Molecular Cloning. Cold Spring Harbor Laboratory Press, Plainview, N.Y. (1989).

Lysate Preparation

5   Untreated rabbit reticulocyte lysate (Ambion) are assembled according to the manufacturer's directions. dsRNA is incubated in the lysate at 30° C for 10 min prior to the addition of mRNAs. Then NOVX mRNAs are added and the incubation continued for an additional 60 min. The molar ratio of double stranded RNA and mRNA is about 200:1. The NOVX mRNA is radiolabeled (using known techniques) and its stability is monitored by gel electrophoresis.

10   In a parallel experiment made with the same conditions, the double stranded RNA is internally radiolabeled with a ^{32}P-ATP. Reactions are stopped by the addition of 2 X proteinase K buffer and deproteinized as described previously (Tuschl *et al.*, Genes Dev., 13:3191-3197 (1999)). Products are analyzed by electrophoresis in 15% or 18% polyacrylamide sequencing gels using appropriate RNA standards. By monitoring the gels
15   for radioactivity, the natural production of 10 to 25 nt RNAs from the double stranded RNA can be determined.

The band of double stranded RNA, about 21-23 bps, is eluded. The efficacy of these 21-23 mers for suppressing NOVX transcription is assayed in vitro using the same rabbit reticulocyte assay described above using 50 nanomolar of double stranded 21-23 mer for
20   each assay. The sequence of these 21-23 mers is then determined using standard nucleic acid sequencing techniques.

RNA Preparation

21 nt RNAs, based on the sequence determined above, are chemically synthesized using Expedite RNA phosphoramidites and thymidine phosphoramidite (Proligo, Germany).
25   Synthetic oligonucleotides are deprotected and gel-purified (Elbashir, Lendeckel, & Tuschl, Genes & Dev. 15, 188-200 (2001)), followed by Sep-Pak C18 cartridge (Waters, Milford, Mass., USA) purification (Tuschl, *et al.*, Biochemistry, 32:11658-11668 (1993)).

These RNAs (20 µM) single strands are incubated in annealing buffer (100 mM potassium acetate, 30 mM HEPES-KOH at pH 7.4, 2 mM magnesium acetate) for 1 min at
30   90° C followed by 1 h at 37° C.

Cell Culture

A cell culture known in the art to regularly express NOVX is propagated using standard conditions. 24 hours before transfection, at approx. 80% confluency, the cells are trypsinized and diluted 1:5 with fresh medium without antibiotics (1-3 X 105 cells/ml) and
5 transferred to 24-well plates (500 ml/well). Transfection is performed using a commercially available lipofection kit and NOVX expression is monitored using standard techniques with positive and negative control. A positive control is cells that naturally express NOVX while a negative control is cells that do not express NOVX. Base-paired 21 and 22 nt siRNAs with overhanging 3' ends mediate efficient sequence-specific mRNA degradation in lysates
10 and in cell culture. Different concentrations of siRNAs are used. An efficient concentration for suppression in vitro in mammalian culture is between 25 nM to 100 nM final concentration. This indicates that siRNAs are effective at concentrations that are several orders of magnitude below the concentrations applied in conventional antisense or ribozyme gene targeting experiments.

15 The above method provides a way both for the deduction of NOVX siRNA sequence and the use of such siRNA for in vitro suppression. In vivo suppression may be performed using the same siRNA using well known in vivo transfection or gene therapy transfection techniques.

20 **Antisense Nucleic Acids**

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a
25 nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein (*e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence). In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire NOVX coding strand, or to only a portion
30 thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a NOVX protein of SEQ ID NO:2n, wherein n is an integer between 1 and 127, or antisense

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nucleic acids complementary to a NOVX nucleic acid sequence of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding a NOVX protein. The term

5 "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding the NOVX protein. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to

10 as 5' and 3' untranslated regions).

Given the coding strand sequences encoding the NOVX protein disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of NOVX mRNA, but more preferably is an

15 oligonucleotide that is antisense to only a portion of the coding or noncoding region of NOVX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of NOVX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or

20 enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally-occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids (*e.g.*, phosphorothioate derivatives

25 and acridine substituted nucleotides can be used).

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-carboxymethylaminomethyl-2-thiouridine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyluracil, dihydrouracil,

30 beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 5-methoxyuracil, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine,

5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, 2-thiouracil, 4-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 5-methyluracil,

5   uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of

10   interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a NOVX protein to thereby inhibit expression of the protein (*e.g.*, by inhibiting transcription and/or translation). The hybridization can be by conventional

15   nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and

20   then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface (*e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens). The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve

25   sufficient nucleic acid molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to. the usual β-units,

30   the strands run parallel to each other. *See, e.g.*, Gaultier, *et al.*, 1987. *Nucl. Acids Res.* **15**: 6625-6641. The antisense nucleic acid molecule can also comprise a

2'-o-methylribonucleotide (*See, e.g.,* Inoue, *et al.* 1987. *Nucl. Acids Res.* 15: 6131-6148) or a chimeric RNA-DNA analogue (*See, e.g.,* Inoue, *et al.,* 1987. *FEBS Lett.* 215: 327-330.

Ribozymes and PNA Moieties

Nucleic acid modifications include, by way of non-limiting example, modified
5   bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In one embodiment, an antisense nucleic acid of the invention is a ribozyme.
10   Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.,* hammerhead ribozymes as described in Haselhoff and Gerlach 1988. *Nature* 334: 585-591) can be used to catalytically cleave NOVX mRNA transcripts to thereby inhibit translation of NOVX mRNA. A ribozyme
15   having specificity for a NOVX-encoding nucleic acid can be designed based upon the nucleotide sequence of a NOVX cDNA disclosed herein (*i.e.,* SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a NOVX-encoding mRNA. *See,*
20   *e.g.,* U.S. Patent 4,987,071 to Cech, *et al.* and U.S. Patent 5,116,742 to Cech, *et al.* NOVX mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. *See, e.g.,* Bartel *et al.,* (1993) *Science* 261:1411-1418.

Alternatively, NOVX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the NOVX nucleic acid (*e.g.,* the
25   NOVX promoter and/or enhancers) to form triple helical structures that prevent transcription of the NOVX gene in target cells. *See, e.g.,* Helene, 1991. *Anticancer Drug Des.* 6: 569-84; Helene, *et al.* 1992. *Ann. N.Y. Acad. Sci.* 660: 27-36; Maher, 1992. *Bioassays* 14: 807-15.

In various embodiments, the NOVX nucleic acids can be modified at the base
30   moiety, sugar moiety or phosphate backbone to improve, *e.g.,* the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic

acids can be modified to generate peptide nucleic acids. *See, e.g.,* Hyrup, *et al.,* 1996. *Bioorg Med Chem* 4: 5-23. As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (*e.g.,* DNA mimics) in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleotide

5   bases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomer can be performed using standard solid phase peptide synthesis protocols as described in Hyrup, *et al.,* 1996, *supra*; Perry-O'Keefe, *et al.,* 1996, *Proc. Natl. Acad. Sci. USA* 93: 14670-14675.

10   PNAs of NOVX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.,* inducing transcription or translation arrest or inhibiting replication. PNAs of NOVX can also be used, for example, in the analysis of single base pair mutations in a gene (*e.g.,* PNA directed PCR clamping; as artificial

15   restriction enzymes when used in combination with other enzymes, *e.g.,* S_1 nucleases (*See,* Hyrup, *et al.,* 1996,*supra*); or as probes or primers for DNA sequence and hybridization (*See,* Hyrup, *et al.,* 1996, *supra*; Perry-O'Keefe, *et al.,* 1996, *supra*).

In another embodiment, PNAs of NOVX can be modified, *e.g.,* to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the

20   formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of NOVX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (*e.g.,* RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity.

25   PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleotide bases, and orientation (*see,* Hyrup, *et al.,* 1996, *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup, *et al.,* 1996, *supra* and Finn, *et al.,* 1996, *Nucl Acids Res* 24: 3357-3363. For example, a DNA chain can be synthesized on a solid support using standard

30   phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.,* 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA. *See, e.g.,* Mag, *et al.,* 1989. *Nucl Acid Res* 17: 5973-5988.

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PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment. *See, e.g.,* Finn, *et al.,* 1996, *supra.* Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. *See, e.g.,* Petersen, *et al.,* 1975. *Bioorg. Med. Chem. Lett.* 5: 1119-11124.

5   In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.,* for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (*see, e.g.,* Letsinger, *et al.,* 1989. *Proc. Natl. Acad. Sci. U.S.A.* 86: 6553-6556; Lemaitre, *et al.,* 1987. *Proc. Natl. Acad. Sci.* 84: 648-652; PCT Publication No. WO88/09810) or the blood-brain barrier (*see, e.g.,* PCT Publication No. WO 89/10134). In
10   addition, oligonucleotides can be modified with hybridization triggered cleavage agents (*see, e.g.,* Krol, *et al.,* 1988. *BioTechniques* 6:958-976) or intercalating agents (*see, e.g.,* Zon, 1988. *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.,* a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

15   **NOVX Polypeptides**

A polypeptide according to the invention includes a polypeptide including the amino acid sequence of NOVX polypeptides whose sequences are provided in any one of SEQ ID NO:2n, wherein n is an integer between 1 and 127. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues
20   shown in any one of SEQ ID NO:2n, wherein n is an integer between 1 and 127, while still encoding a protein that maintains its NOVX activities and physiological functions, or a functional fragment thereof.

In general, a NOVX variant that preserves NOVX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other
25   amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

30   One aspect of the invention pertains to isolated NOVX proteins, and biologically-active portions thereof, or derivatives, fragments, analogs or homologs thereof.

Also provided are polypeptide fragments suitable for use as immunogens to raise anti-NOVX antibodies. In one embodiment, native NOVX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, NOVX proteins are produced by

5   recombinant DNA techniques. Alternative to recombinant expression, a NOVX protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" polypeptide or protein or biologically-active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the NOVX protein is derived, or substantially free from

10   chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of NOVX proteins in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly-produced. In one embodiment, the language "substantially free of cellular material" includes preparations of NOVX proteins having less than about 30% (by dry

15   weight) of non-NOVX proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-NOVX proteins, still more preferably less than about 10% of non-NOVX proteins, and most preferably less than about 5% of non-NOVX proteins. When the NOVX protein or biologically-active portion thereof is recombinantly-produced, it is also preferably substantially free of culture medium, *i.e.*,

20   culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the NOVX protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the

25   language "substantially free of chemical precursors or other chemicals" includes preparations of NOVX proteins having less than about 30% (by dry weight) of chemical precursors or non-NOVX chemicals, more preferably less than about 20% chemical precursors or non-NOVX chemicals, still more preferably less than about 10% chemical precursors or non-NOVX chemicals, and most preferably less than about 5% chemical

30   precursors or non-NOVX chemicals.

Biologically-active portions of NOVX proteins include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of the

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NOVX proteins (*e.g.*, the amino acid sequence of SEQ ID NO:2*n*, wherein *n* is an integer between 1 and 127) that include fewer amino acids than the full-length NOVX proteins, and exhibit at least one activity of a NOVX protein. Typically, biologically-active portions comprise a domain or motif with at least one activity of the NOVX protein. A

5   biologically-active portion of a NOVX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acid residues in length.

Moreover, other biologically-active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native NOVX protein.

10   In an embodiment, the NOVX protein has an amino acid sequence of SEQ ID NO:2*n*, wherein *n* is an integer between 1 and 127. In other embodiments, the NOVX protein is substantially homologous to SEQ ID NO:2*n*, wherein *n* is an integer between 1 and 127, and retains the functional activity of the protein of SEQ ID NO:2*n*, wherein *n* is an integer between 1 and 127, yet differs in amino acid sequence due to natural allelic variation

15   or mutagenesis, as described in detail, below. Accordingly, in another embodiment, the NOVX protein is a protein that comprises an amino acid sequence at least about 45% homologous to the amino acid sequence of SEQ ID NO:2*n*, wherein *n* is an integer between 1 and 127, and retains the functional activity of the NOVX proteins of SEQ ID NO:2*n*, wherein *n* is an integer between 1 and 127.

20   **Determining Homology Between Two or More Sequences**

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or

25   nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

30   The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs

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known in the art, such as GAP software provided in the GCG program package. *See,*
Needleman and Wunsch, 1970. *J Mol Biol* 48: 443-453. Using GCG GAP software with
the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0
and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid
5   sequences referred to above exhibits a degree of identity preferably of at least 70%, 75%,
80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence of
SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127.

The term "sequence identity" refers to the degree to which two polynucleotide or
polypeptide sequences are identical on a residue-by-residue basis over a particular region of
10   comparison. The term "percentage of sequence identity" is calculated by comparing two
optimally aligned sequences over that region of comparison, determining the number of
positions at which the identical nucleic acid base (*e.g.,* A, T, C, G, U, or I, in the case of
nucleic acids) occurs in both sequences to yield the number of matched positions, dividing
the number of matched positions by the total number of positions in the region of
15   comparison (*i.e.,* the window size), and multiplying the result by 100 to yield the percentage
of sequence identity. The term "substantial identity" as used herein denotes a characteristic
of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at
least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95
percent sequence identity, more usually at least 99 percent sequence identity as compared to
20   a reference sequence over a comparison region.

Chimeric and Fusion Proteins

The invention also provides NOVX chimeric or fusion proteins. As used herein, a
NOVX "chimeric protein" or "fusion protein" comprises a NOVX polypeptide
operatively-linked to a non-NOVX polypeptide. An "NOVX polypeptide" refers to a
25   polypeptide having an amino acid sequence corresponding to a NOVX protein of SEQ ID
NO:$2n$, wherein n is an integer between 1 and 127, whereas a "non-NOVX polypeptide"
refers to a polypeptide having an amino acid sequence corresponding to a protein that is not
substantially homologous to the NOVX protein, *e.g.,* a protein that is different from the
NOVX protein and that is derived from the same or a different organism. Within a NOVX
30   fusion protein the NOVX polypeptide can correspond to all or a portion of a NOVX protein.
In one embodiment, a NOVX fusion protein comprises at least one biologically-active
portion of a NOVX protein. In another embodiment, a NOVX fusion protein comprises at

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least two biologically-active portions of a NOVX protein. In yet another embodiment, a NOVX fusion protein comprises at least three biologically-active portions of a NOVX protein. Within the fusion protein, the term "operatively-linked" is intended to indicate that the NOVX polypeptide and the non-NOVX polypeptide are fused in-frame with one

5   another. The non-NOVX polypeptide can be fused to the N-terminus or C-terminus of the NOVX polypeptide.

In one embodiment, the fusion protein is a GST-NOVX fusion protein in which the NOVX sequences are fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant NOVX

10   polypeptides.   ,

In another embodiment, the fusion protein is a NOVX protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of NOVX can be increased through use of a heterologous signal sequence.

15   In yet another embodiment, the fusion protein is a NOVX-immunoglobulin fusion protein in which the NOVX sequences are fused to sequences derived from a member of the immunoglobulin protein family. The NOVX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a NOVX ligand and a NOVX protein on the

20   surface of a cell, to thereby suppress NOVX-mediated signal transduction *in vivo*. The
.   NOVX-immunoglobulin fusion proteins can be used to affect the bioavailability of a NOVX cognate ligand. Inhibition of the NOVX ligand/NOVX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the

25   NOVX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-NOVX antibodies in a subject, to purify NOVX ligands, and in screening assays to identify molecules that inhibit the interaction of NOVX with a NOVX ligand.

A NOVX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different

30   polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as

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appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic
ligation. In another embodiment, the fusion gene can be synthesized by conventional
techniques including automated DNA synthesizers. Alternatively, PCR amplification of
gene fragments can be carried out using anchor primers that give rise to complementary

5   overhangs between two consecutive gene fragments that can subsequently be annealed and
reamplified to generate a chimeric gene sequence (*see, e.g.*, Ausubel, *et al.* (eds.) CURRENT
PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many
expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a
GST polypeptide). A NOVX-encoding nucleic acid can be cloned into such an expression

10   vector such that the fusion moiety is linked in-frame to the NOVX protein.

NOVX Agonists and Antagonists

The invention also pertains to variants of the NOVX proteins that function as either
NOVX agonists (*i.e.*, mimetics) or as NOVX antagonists. Variants of the NOVX protein
can be generated by mutagenesis (*e.g.*, discrete point mutation or truncation of the NOVX

15   protein). An agonist of the NOVX protein can retain substantially the same, or a subset of,
the biological activities of the naturally occurring form of the NOVX protein. An
antagonist of the NOVX protein can inhibit one or more of the activities of the naturally
occurring form of the NOVX protein by, for example, competitively binding to a
downstream or upstream member of a cellular signaling cascade which includes the NOVX

20   protein. Thus, specific biological effects can be elicited by treatment with a variant of
limited function. In one embodiment, treatment of a subject with a variant having a subset
of the biological activities of the naturally occurring form of the protein has fewer side
effects in a subject relative to treatment with the naturally occurring form of the NOVX
proteins.

25   Variants of the NOVX proteins that function as either NOVX agonists (*i.e.*,
mimetics) or as NOVX antagonists can be identified by screening combinatorial libraries of
mutants (*e.g.*, truncation mutants) of the NOVX proteins for NOVX protein agonist or
antagonist activity. In one embodiment, a variegated library of NOVX variants is generated
by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene

30   library. A variegated library of NOVX variants can be produced by, for example,
enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that
a degenerate set of potential NOVX sequences is expressible as individual polypeptides, or

alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of NOVX sequences therein. There are a variety of methods which can be used to produce libraries of potential NOVX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA

5   synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential NOVX sequences. Methods for synthesizing degenerate oligonucleotides are well-known within the art. *See, e.g.,* Narang, 1983. *Tetrahedron* 39: 3; Itakura, *et al.,* 1984. *Annu. Rev. Biochem.* 53: 323; Itakura, *et al.,* 1984.

10   *Science* 198: 1056; Ike, *et al.,* 1983. *Nucl. Acids Res.* 11: 477.

Polypeptide Libraries

In addition, libraries of fragments of the NOVX protein coding sequences can be used to generate a variegated population of NOVX fragments for screening and subsequent selection of variants of a NOVX protein. In one embodiment, a library of coding sequence

15   fragments can be generated by treating a double stranded PCR fragment of a NOVX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double-stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S₁ nuclease,

20   and ligating the resulting fragment library into an expression vector. By this method, expression libraries can be derived which encodes N-terminal and internal fragments of various sizes of the NOVX proteins.

Various techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA

25   libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of NOVX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of

30   vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the

frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify NOVX variants. *See, e.g.*, Arkin and Youvan, 1992, *Proc. Natl. Acad. Sci. USA* 89: 7811-7815; Delgrave, *et al.*, 1993. *Protein Engineering* 6:327-331.

Anti-NOVX Antibodies

5   Included in the invention are antibodies to NOVX proteins, or fragments of NOVX proteins. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin (Ig) molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single

10   chain, F_{ab}, $F_{ab'}$ and $F_{(ab')2}$ fragments, and an F_{ab} expression library. In general, antibody molecules obtained from humans relates to any of the classes IgG, IgM, IgA, IgE and IgD, which differ from one another by the nature of the heavy chain present in the molecule. Certain classes have subclasses as well, such as IgG_1, IgG_2, and others. Furthermore, in humans, the light chain may be a kappa chain or a lambda chain. Reference herein to

15   antibodies includes a reference to all such classes, subclasses and types of human antibody species.

       An isolated protein of the invention intended to serve as an antigen, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that immunospecifically bind the antigen, using standard techniques for polyclonal and

20   monoclonal antibody preparation. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments of the antigen for use as immunogens. An antigenic peptide fragment comprises at least 6 amino acid residues of the amino acid sequence of the full length protein, such as an amino acid sequence of SEQ ID NO:2*n*, wherein *n* is an integer between 1 and 127, and encompasses an epitope thereof such that an

25   antibody raised against the peptide forms a specific immune complex with the full length protein or with any fragment that contains the epitope. Preferably, the antigenic peptide comprises at least 10 amino acid residues, or at least 15 amino acid residues, or at least 20 amino acid residues, or at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of the protein that are located on its surface; commonly

30   these are hydrophilic regions.

In certain embodiments of the invention, at least one epitope encompassed by the antigenic peptide is a region of NOVX that is located on the surface of the protein, *e.g.*, a hydrophilic region. A hydrophobicity analysis of the human NOVX protein sequence will indicate which regions of a NOVX polypeptide are particularly hydrophilic and, therefore,

5   are likely to encode surface residues useful for targeting antibody production. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. *See, e.g.*, Hopp and Woods, 1981, *Proc. Nat. Acad. Sci. USA* 78:

10   3824-3828; Kyte and Doolittle 1982, *J. Mol. Biol.* 157: 105-142, each incorporated herein by reference in their entirety. Antibodies that are specific for one or more domains within an antigenic protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

The term "epitope" includes any protein determinant capable of specific binding to

15   an immunoglobulin or T-cell receptor. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. A NOVX polypeptide or a fragment thereof comprises at least one antigenic epitope. An anti-NOVX antibody of the present invention is said to specifically bind to

20   antigen NOVX when the equilibrium binding constant (K_D) is ≤ 1 μM, preferably ≤ 100 nM, more preferably ≤ 10 nM, and most preferably ≤ 100 pM to about 1 pM, as measured by assays such as radioligand binding assays or similar assays known to those skilled in the art.

A protein of the invention, or a derivative, fragment, analog, homolog or ortholog thereof, may be utilized as an immunogen in the generation of antibodies that

25   immunospecifically bind these protein components.

Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies directed against a protein of the invention, or against derivatives, fragments, analogs homologs or orthologs thereof (*see,* for example, Antibodies: A Laboratory Manual, Harlow E, and Lane D, 1988, Cold Spring Harbor

30   Laboratory Press, Cold Spring Harbor, NY, incorporated herein by reference). Some of these antibodies are discussed below.

Polyclonal Antibodies

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by one or more injections with the native protein, a synthetic variant thereof, or a derivative of the foregoing. An appropriate

5   immunogenic preparation can contain, for example, the naturally occurring immunogenic protein, a chemically synthesized polypeptide representing the immunogenic protein, or a recombinantly expressed immunogenic protein. Furthermore, the protein may be conjugated to a second protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet

10 hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), adjuvants usable

15 in humans such as Bacille Calmette-Guerin and Corynebacterium parvum, or similar immunostimulatory agents. Additional examples of adjuvants which can be employed include MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

The polyclonal antibody molecules directed against the immunogenic protein can be

20 isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as affinity chromatography using protein A or protein G, which provide primarily the IgG fraction of immune serum. Subsequently, or alternatively, the specific antigen which is the target of the immunoglobulin sought, or an epitope thereof, may be immobilized on a column to purify the immune specific antibody by immunoaffinity

25 chromatography. Purification of immunoglobulins is discussed, for example, by D. Wilkinson (The Scientist, published by The Scientist, Inc., Philadelphia PA, Vol. 14, No. 8 (April 17, 2000), pp. 25-28).

Monoclonal Antibodies

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The term "monoclonal antibody" (MAb) or "monoclonal antibody composition", as

30 used herein, refers to a population of antibody molecules that contain only one molecular species of antibody molecule consisting of a unique light chain gene product and a unique

heavy chain gene product. In particular, the complementarity determining regions (CDRs) of the monoclonal antibody are identical in all the molecules of the population. MAbs thus contain an antigen binding site capable of immunoreacting with a particular epitope of the antigen characterized by a unique binding affinity for it.

5   Monoclonal antibodies can be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes can be
10   immunized in vitro.

The immunizing agent will typically include the protein antigen, a fragment thereof or a fusion protein thereof. Generally, either peripheral blood lymphocytes are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell
15   line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells can be cultured in a suitable culture medium that
20   preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

25   Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas,
30   Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J. Immunol.,

133:3001 (1984); Brodeur *et al.*, Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against the antigen. Preferably, the

5   binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980). It is an

10   objective, especially important in therapeutic applications of monoclonal antibodies, to identify antibodies having a high degree of specificity and a high binding affinity for the target antigen.

After the desired hybridoma cells are identified, the clones can be subcloned by limiting dilution procedures and grown by standard methods (Goding,1986). Suitable

15   culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells can be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones can be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification

20   procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies can also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (*e.g.*, by

25   using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA can be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce

30   immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the

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homologous murine sequences (U.S. Patent No. 4,816,567; Morrison, Nature 368, 812-13
(1994)) or by covalently joining to the immunoglobulin coding sequence all or part of the
coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin
polypeptide can be substituted for the constant domains of an antibody of the invention, or
5   can be substituted for the variable domains of one antigen-combining site of an antibody of
the invention to create a chimeric bivalent antibody.

Humanized Antibodies

The antibodies directed against the protein antigens of the invention can further
comprise humanized antibodies or human antibodies. These antibodies are suitable for
10   administration to humans without engendering an immune response by the human against
the administered immunoglobulin. Humanized forms of antibodies are chimeric
immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab',
$F(ab')_2$ or other antigen-binding subsequences of antibodies) that are principally comprised
of the sequence of a human immunoglobulin, and contain minimal sequence derived from a
15   non-human immunoglobulin. Humanization can be performed following the method of
Winter and co-workers (Jones *et al.*, Nature, 321:522-525 (1986); Riechmann *et al.*, Nature,
332:323-327 (1988); Verhoeyen *et al.*, Science, 239:1534-1536 (1988)), by substituting
rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. (See
also U.S. Patent No. 5,225,539.) In some instances, Fv framework residues of the human
20   immunoglobulin are replaced by corresponding non-human residues. Humanized
antibodies can also comprise residues which are found neither in the recipient antibody nor
in the imported CDR or framework sequences. In general, the humanized antibody will
comprise substantially all of at least one, and typically two, variable domains, in which all
or substantially all of the CDR regions correspond to those of a non-human
25   immunoglobulin and all or substantially all of the framework regions are those of a human
immunoglobulin consensus sequence. The humanized antibody optimally also will
comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a
human immunoglobulin (Jones *et al.*, 1986; Riechmann *et al.*, 1988; and Presta, Curr. Op.
Struct. Biol., 2:593-596 (1992)).

Human Antibodies

Fully human antibodies essentially relate to antibody molecules in which the entire sequence of both the light chain and the heavy chain, including the CDRs, arise from human genes. Such antibodies are termed "human antibodies", or "fully human antibodies" herein.

5   Human monoclonal antibodies can be prepared by the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 Immunol Today 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be

10   produced by using human hybridomas (see Cote, *et al.*, 1983. Proc Natl Acad Sci USA 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus in vitro (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

In addition, human antibodies can also be produced using additional techniques,

15   including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks *et al.*, J. Mol. Biol., 222:581 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in

20   humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in Marks *et al.* (Bio/Technology 10, 779-783 (1992)); Lonberg *et al.* (Nature 368 856-859 (1994)); Morrison (Nature 368, 812-13 (1994)); Fishwild et al,(Nature Biotechnology 14, 845-51 (1996)); Neuberger

25   (Nature Biotechnology 14, 826 (1996)); and Lonberg and Huszar (Intern. Rev. Immunol. 13 65-93 (1995)).

Human antibodies may additionally be produced using transgenic nonhuman animals which are modified so as to produce fully human antibodies rather than the animal's endogenous antibodies in response to challenge by an antigen. (See PCT

30   publication WO94/02602). The endogenous genes encoding the heavy and light immunoglobulin chains in the nonhuman host have been incapacitated, and active loci encoding human heavy and light chain immunoglobulins are inserted into the host's

genome. The human genes are incorporated, for example, using yeast artificial chromosomes containing the requisite human DNA segments. An animal which provides all the desired modifications is then obtained as progeny by crossbreeding intermediate transgenic animals containing fewer than the full complement of the modifications. The

5   preferred embodiment of such a nonhuman animal is a mouse, and is termed the Xenomouse™ as disclosed in PCT publications WO 96/33735 and WO 96/34096. This animal produces B cells which secrete fully human immunoglobulins. The antibodies can be obtained directly from the animal after immunization with an immunogen of interest, as, for example, a preparation of a polyclonal antibody, or alternatively from immortalized B

10   cells derived from the animal, such as hybridomas producing monoclonal antibodies. Additionally, the genes encoding the immunoglobulins with human variable regions can be recovered and expressed to obtain the antibodies directly, or can be further modified to obtain analogs of antibodies such as, for example, single chain Fv molecules.

An example of a method of producing a nonhuman host, exemplified as a mouse,

15   lacking expression of an endogenous immunoglobulin heavy chain is disclosed in U.S. Patent No. 5,939,598. It can be obtained by a method including deleting the J segment genes from at least one endogenous heavy chain locus in an embryonic stem cell to prevent rearrangement of the locus and to prevent formation of a transcript of a rearranged immunoglobulin heavy chain locus, the deletion being effected by a targeting vector

20   containing a gene encoding a selectable marker; and producing from the embryonic stem cell a transgenic mouse whose somatic and germ cells contain the gene encoding the selectable marker.

A method for producing an antibody of interest, such as a human antibody, is disclosed in U.S. Patent No. 5,916,771. It includes introducing an expression vector that

25   contains a nucleotide sequence encoding a heavy chain into one mammalian host cell in culture, introducing an expression vector containing a nucleotide sequence encoding a light chain into another mammalian host cell, and fusing the two cells to form a hybrid cell. The hybrid cell expresses an antibody containing the heavy chain and the light chain.

In a further improvement on this procedure, a method for identifying a clinically

30   relevant epitope on an immunogen, and a correlative method for selecting an antibody that binds immunospecifically to the relevant epitope with high affinity, are disclosed in PCT publication WO 99/53049.

F$_{ab}$ Fragments and Single Chain Antibodies

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to an antigenic protein of the invention (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F$_{ab}$ expression

5   libraries (see *e.g.*, Huse, *et al.*, 1989 Science 246: 1275-1281) to allow rapid and effective identification of monoclonal F$_{ab}$ fragments with the desired specificity for a protein or derivatives, fragments, analogs or homologs thereof. Antibody fragments that contain the idiotypes to a protein antigen may be produced by techniques known in the art including, but not limited to: (i) an F$_{(ab')2}$ fragment produced by pepsin digestion of an antibody

10   molecule; (ii) an F$_{ab}$ fragment generated by reducing the disulfide bridges of an F$_{(ab')2}$ fragment; (iii) an F$_{ab}$ fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F$_v$ fragments.

Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies

15   that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for an antigenic protein of the invention. The second binding target is any other antigen, and advantageously is a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the

20   recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the

25   correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen

30   combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part

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of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are

5   co-transfected into a suitable host organism. For further details of generating bispecific antibodies *see*, for example, Suresh *et al.*, Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at

10   least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or

15   threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (*e.g.* F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies

20   can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives.

25   One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Additionally, Fab' fragments can be directly recovered from E. coli and chemically

30   coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from E. coli and subjected to directed chemical

coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

5   Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were

10   reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a

15   light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. *See,* Gruber *et*

20   *al.*, J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies can bind to two different epitopes, at least one of which originates in the protein antigen of the invention. Alternatively, an anti-antigenic arm

25   of an immunoglobulin molecule can be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular antigen. Bispecific antibodies can also be used to direct cytotoxic agents to cells which express a

30   particular antigen. These antibodies possess an antigen-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or

TETA. Another bispecific antibody of interest binds the protein antigen described herein and further binds tissue factor (TF).

Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention.

5   Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980), and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking

10   agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

Effector Function Engineering

15   It can be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) can be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased

20   complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual

25   Fc regions and can thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an

enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments
thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have
been described above. Enzymatically active toxins and fragments thereof that can be used
5   include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A
chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain,
alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins
(PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria
officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the
10   tricothecenes. A variety of radionuclides are available for the production of
radioconjugated antibodies. Examples include ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of
bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate
(SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl
15   adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as
glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine),
bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine),
diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such
as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as
20   described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled
1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an
exemplary chelating agent for conjugation of radionucleotide to the antibody. See
WO94/11026.

In another embodiment, the antibody can be conjugated to a "receptor" (such
25   streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is
administered to the patient, followed by removal of unbound conjugate from the circulation
using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is in turn
conjugated to a cytotoxic agent.

Immunoliposomes

30   The antibodies disclosed herein can also be formulated as immunoliposomes.
Liposomes containing the antibody are prepared by methods known in the art, such as

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described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

5   Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al .,J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A

10   chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

Diagnostic Applications of Antibodies Directed Against the Proteins of the Invention

         In one embodiment, methods for the screening of antibodies that possess the desired

15   specificity include, but are not limited to, enzyme linked immunosorbent assay (ELISA) and other immunologically mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of an NOVX protein is facilitated by generation of hybridomas that bind to the fragment of an NOVX protein possessing such a domain. Thus, antibodies that are specific for a desired domain

20   within an NOVX protein, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

         Antibodies directed against a NOVX protein of the invention may be used in methods known within the art relating to the localization and/or quantitation of a NOVX protein (*e.g.*, for use in measuring levels of the NOVX protein within appropriate

25   physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies specific to a NOVX protein, or derivative, fragment, analog or homolog thereof, that contain the antibody derived antigen binding domain, are utilized as pharmacologically active compounds (referred to hereinafter as "Therapeutics").

30   An antibody specific for a NOVX protein of the invention (e.g., a monoclonal antibody or a polyclonal antibody) can be used to isolate a NOVX polypeptide by standard

techniques, such as immunoaffinity, chromatography or immunoprecipitation. An antibody to a NOVX polypeptide can facilitate the purification of a natural NOVX antigen from cells, or of a recombinantly produced NOVX antigen expressed in host cells. Moreover, such an anti-NOVX antibody can be used to detect the antigenic NOVX protein (*e.g.*, in a cellular

5   lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the antigenic NOVX protein. Antibodies directed against a NOVX protein can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance.

10   Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials

15   include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

20   **Antibody Therapeutics**

         Antibodies of the invention, including polyclonal, monoclonal, humanized and fully human antibodies, may used as therapeutic agents. Such agents will generally be employed to treat or prevent a disease or pathology in a subject. An antibody preparation, preferably one having high specificity and high affinity for its target antigen, is administered to the

25   subject and will generally have an effect due to its binding with the target. Such an effect may be one of two kinds, depending on the specific nature of the interaction between the given antibody molecule and the target antigen in question. In the first instance, administration of the antibody may abrogate or inhibit the binding of the target with an endogenous ligand to which it naturally binds. In this case, the antibody binds to the target

30   and masks a binding site of the naturally occurring ligand, wherein the ligand serves as an effector molecule. Thus the receptor mediates a signal transduction pathway for which ligand is responsible.

Alternatively, the effect may be one in which the antibody elicits a physiological result by virtue of binding to an effector binding site on the target molecule. In this case the target, a receptor having an endogenous ligand which may be absent or defective in the disease or pathology, binds the antibody as a surrogate effector ligand, initiating a

5   receptor-based signal transduction event by the receptor.

A therapeutically effective amount of an antibody of the invention relates generally to the amount needed to achieve a therapeutic objective. As noted above, this may be a binding interaction between the antibody and its target antigen that, in certain cases, interferes with the functioning of the target, and in other cases, promotes a physiological

10   response. The amount required to be administered will furthermore depend on the binding affinity of the antibody for its specific antigen, and will also depend on the rate at which an administered antibody is depleted from the free volume other subject to which it is administered. Common ranges for therapeutically effective dosing of an antibody or antibody fragment of the invention may be, by way of nonlimiting example, from about 0.1

15   mg/kg body weight to about 50 mg/kg body weight. Common dosing frequencies may range, for example, from twice daily to once a week.

Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a protein of the invention, as well as other molecules identified by the screening assays disclosed herein, can be administered for the treatment of

20   various disorders in the form of pharmaceutical compositions. Principles and considerations involved in preparing such compositions, as well as guidance in the choice of components are provided, for example, in Remington: The Science And Practice Of Pharmacy 19th ed. (Alfonso R. Gennaro, *et al.*, editors) Mack Pub. Co., Easton, Pa.: 1995; Drug Absorption Enhancement: Concepts, Possibilities, Limitations, And Trends, Harwood

25   Academic Publishers, Langhorne, Pa., 1994; and Peptide And Protein Drug Delivery (Advances In Parenteral Sciences, Vol. 4), 1991, M. Dekker, New York.

If the antigenic protein is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the

30   smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody,

peptide molecules can be designed that retain the ability to bind the target protein sequence.
Such peptides can be synthesized chemically and/or produced by recombinant DNA
technology. *See, e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993).
The formulation herein can also contain more than one active compound as necessary for
5   the particular indication being treated, preferably those with complementary activities that
do not adversely affect each other. Alternatively, or in addition, the composition can
comprise an agent that enhances its function, such as, for example, a cytotoxic agent,
cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably
present in combination in amounts that are effective for the purpose intended.

10   The active ingredients can also be entrapped in microcapsules prepared, for
example, by coacervation techniques or by interfacial polymerization, for example,
hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate)
microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes,
albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in
15   macroemulsions.

The formulations to be used for in vivo administration must be sterile. This is
readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations can be prepared. Suitable examples of
sustained-release preparations include semipermeable matrices of solid hydrophobic
20   polymers containing the antibody, which matrices are in the form of shaped articles, e.g.,
films, or microcapsules. Examples of sustained-release matrices include polyesters,
hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)),
polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ
ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic
25   acid copolymers such as the LUPRON DEPOT ™ (injectable microspheres composed of
lactic acid-glycolic acid copolymer and leuprolide acetate), and
poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic
acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release
proteins for shorter time periods.

ELISA Assay

An agent for detecting an analyte protein is an antibody capable of binding to an
analyte protein, preferably an antibody with a detectable label. Antibodies can be
polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*,
5   F_{ab} or $F_{(ab)2}$) can be used. The term "labeled", with regard to the probe or antibody, is
intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically
linking) a detectable substance to the probe or antibody, as well as indirect labeling of the
probe or antibody by reactivity with another reagent that is directly labeled. Examples of
indirect labeling include detection of a primary antibody using a fluorescently-labeled
10   secondary antibody and end-labeling of a DNA probe with biotin such that it can be
detected with fluorescently-labeled streptavidin. The term "biological sample" is intended
to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells
and fluids present within a subject. Included within the usage of the term "biological
sample", therefore, is blood and a fraction or component of blood including blood serum,
15   blood plasma, or lymph. That is, the detection method of the invention can be used to
detect an analyte mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as
in vivo. For example, *in vitro* techniques for detection of an analyte mRNA include
Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of an
analyte protein include enzyme linked immunosorbent assays (ELISAs), Western blots,
20   immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of an
analyte genomic DNA include Southern hybridizations. Procedures for conducting
immunoassays are described, for example in "ELISA: Theory and Practice: Methods in
Molecular Biology", Vol. 42, J. R. Crowther (Ed.) Human Press, Totowa, NJ, 1995;
"Immunoassay", E. Diamandis and T. Christopoulus, Academic Press, Inc., San Diego, CA,
25   1996; and "Practice and Thory of Enzyme Immunoassays", P. Tijssen, Elsevier Science
Publishers, Amsterdam, 1985. Furthermore, *in vivo* techniques for detection of an analyte
protein include introducing into a subject a labeled anti-an analyte protein antibody. For
example, the antibody can be labeled with a radioactive marker whose presence and
location in a subject can be detected by standard imaging techniques.

NOVX Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a NOVX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule
5   capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors
10   having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors". In general,
15   expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve
20   equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively-linked to the
25   nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably-linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell).

30   The term "regulatory sequence" is intended to includes promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY:

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METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory
sequences include those that direct constitutive expression of a nucleotide sequence in many
types of host cell and those that direct expression of the nucleotide sequence only in certain
host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled

5   in the art that the design of the expression vector can depend on such factors as the choice
of the host cell to be transformed, the level of expression of protein desired, *etc.* The
expression vectors of the invention can be introduced into host cells to thereby produce
proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as
described herein (*e.g.*, NOVX proteins, mutant forms of NOVX proteins, fusion proteins,

10   *etc.*).

The recombinant expression vectors of the invention can be designed for expression
of NOVX proteins in prokaryotic or eukaryotic cells. For example, NOVX proteins can be
expressed in bacterial cells such as *Escherichia coli*, insect cells (using baculovirus
expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further

15   in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic
Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be
transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and
T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *Escherichia coli*

20   with vectors containing constitutive or inducible promoters directing the expression of
either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a
protein encoded therein, usually to the amino terminus of the recombinant protein. Such
fusion vectors typically serve three purposes: (*i*) to increase expression of recombinant
protein; (*ii*) to increase the solubility of the recombinant protein; and (*iii*) to aid in the

25   purification of the recombinant protein by acting as a ligand in affinity purification. Often,
in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the
fusion moiety and the recombinant protein to enable separation of the recombinant protein
from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and
their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical

30   fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988.
Gene 67: 31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia,

Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION
5 TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. *See, e.g.,* Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN
10 ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (*see, e.g.,* Wada, *et al.*, 1992. *Nucl. Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

15 In another embodiment, the NOVX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerivisae* include pYepSec1 (Baldari, *et al.*, 1987. *EMBO J.* 6: 229-234), pMFa (Kurjan and Herskowitz, 1982. *Cell* 30: 933-943), pJRY88 (Schultz *et al.*, 1987. *Gene* 54: 113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

20 Alternatively, NOVX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.,* SF9 cells) include the pAc series (Smith, *et al.*, 1983. *Mol. Cell. Biol.* 3: 2156-2165) and the pVL series (Lucklow and Summers, 1989. *Virology* 170: 31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in
25 mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987. *Nature* 329: 840) and pMT2PC (Kaufman, *et al.*, 1987. *EMBO J.* 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, and simian virus
30 40. For other suitable expression systems for both prokaryotic and eukaryotic cells *see, e.g.,* Chapters 16 and 17 of Sambrook, *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL.

2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring
Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of
directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*,
5   tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific
regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific
promoters include the albumin promoter (liver-specific; Pinkert, *et al.*, 1987. *Genes Dev.* 1:
268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43:
235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO*
10   *J.* 8: 729-733) and immunoglobulins (Banerji, *et al.*, 1983. *Cell* 33: 729-740; Queen and
Baltimore, 1983. *Cell* 33: 741-748), neuron-specific promoters (*e.g.*, the neurofilament
promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477),
pancreas-specific promoters (Edlund, *et al.*, 1985. *Science* 230: 912-916), and mammary
gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European
15   Application Publication No. 264,166). Developmentally-regulated promoters are also
encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss, 1990. *Science* 249:
374-379) and the α-fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3:
537-546).

The invention further provides a recombinant expression vector comprising a DNA
20   molecule of the invention cloned into the expression vector in an antisense orientation. That
is, the DNA molecule is operatively-linked to a regulatory sequence in a manner that allows
for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense
to NOVX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the
antisense orientation can be chosen that direct the continuous expression of the antisense
25   RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or
regulatory sequences can be chosen that direct constitutive, tissue specific or cell type
specific expression of antisense RNA. The antisense expression vector can be in the form
of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are
produced under the control of a high efficiency regulatory region, the activity of which can
30   be determined by the cell type into which the vector is introduced. For a discussion of the
regulation of gene expression using antisense genes *see, e.g.,* Weintraub, *et al.*, "Antisense
RNA as a molecular tool for genetic analysis," *Reviews-Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of

5   such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, NOVX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells

10   (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing

15   foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989),

20   and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is

25   generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding NOVX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*,

30   cells that have incorporated the selectable marker gene will survive, while the other cells die).

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A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) NOVX protein. Accordingly, the invention further provides methods for producing NOVX protein using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a

5 recombinant expression vector encoding NOVX protein has been introduced) in a suitable medium such that NOVX protein is produced. In another embodiment, the method further comprises isolating NOVX protein from the medium or the host cell.

Transgenic NOVX Animals

The host cells of the invention can also be used to produce non-human transgenic

10 animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which NOVX protein-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous NOVX sequences have been introduced into their genome or homologous recombinant animals in which endogenous NOVX sequences have been altered. Such

15 animals are useful for studying the function and/or activity of NOVX protein and for identifying and/or evaluating modulators of NOVX protein activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows,

20 goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a

25 mouse, in which an endogenous NOVX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing NOVX-encoding

30 nucleic acid into the male pronuclei of a fertilized oocyte (e.g., by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal. The human NOVX cDNA sequences, i.e., any one of SEQ ID NO:2n-1, wherein n is an

integer between 1 and 127, can be introduced as a transgene into the genome of a non-human animal. Alternatively, a non-human homolog of the human NOVX gene, such as a mouse NOVX gene, can be isolated based on hybridization to the human NOVX cDNA (described further *supra*) and used as a transgene. Intronic sequences and polyadenylation

5 signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably-linked to the NOVX transgene to direct expression of NOVX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent

10 Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan, 1986. In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the NOVX transgene in its genome and/or expression of NOVX mRNA in tissues or cells of the animals. A transgenic founder animal

15 can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene-encoding NOVX protein can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a NOVX gene into which a deletion, addition or substitution has been

20 introduced to thereby alter, *e.g.*, functionally disrupt, the NOVX gene. The NOVX gene can be a human gene (*e.g.*, the cDNA of any one of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127), but more preferably, is a non-human homolog of a human NOVX gene. For example, a mouse homolog of human NOVX gene of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, can be used to construct a homologous

25 recombination vector suitable for altering an endogenous NOVX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous NOVX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous

30 recombination, the endogenous NOVX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous NOVX protein). In the homologous recombination

vector, the altered portion of the NOVX gene is flanked at its 5'- and 3'-termini by additional nucleic acid of the NOVX gene to allow for homologous recombination to occur between the exogenous NOVX gene carried by the vector and an endogenous NOVX gene in an embryonic stem cell. The additional flanking NOVX nucleic acid is of sufficient

5   length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector. *See, e.g.,* Thomas, *et al.,* 1987. *Cell* 51: 503 for a description of homologous recombination vectors. The vector is ten introduced into an embryonic stem cell line (*e.g.,* by electroporation) and cells in which the introduced NOVX gene has

10   homologously-recombined with the endogenous NOVX gene are selected. *See, e.g.,* Li, *et al.,* 1992. *Cell* 69: 915.

The selected cells are then injected into a blastocyst of an animal (*e.g.,* a mouse) to form aggregation chimeras. *See, e.g.,* Bradley, 1987. In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp.

15   113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors

20   and homologous recombinant animals are described further in Bradley, 1991. *Curr. Opin. Biotechnol.* 2: 823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example

25   of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, *See, e.g.,* Lakso, *et al.,* 1992. *Proc. Natl. Acad. Sci. USA* 89: 6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae. See,* O'Gorman, *et al.,* 1991. *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals

30   containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic

animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, *et al.*, 1997. *Nature* 385: 810-813. In brief,

5   a cell (*e.g.*, a somatic cell) from the transgenic animal can be isolated and induced to exit the growth cycle and enter G_0 phase. The quiescent cell can then be fused, *e.g.*, through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster

10   animal. The offspring borne of this female foster animal will be a clone of the animal from which the cell (*e.g.*, the somatic cell) is isolated.

Pharmaceutical Compositions

The NOVX nucleic acid molecules, NOVX proteins, and anti-NOVX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments,

15   analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying

20   agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles

25   such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

30   A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include

parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (i.e., topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols,

5 glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide.

10 The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration,

15 suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a

20 solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be

25 achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays

30 absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (e.g., a NOVX protein or anti-NOVX antibody) in the required amount in an appropriate

solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the

5   preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral

10   therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The

15   tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring

20   agent such as peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For

25   transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are

30   formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will
5   protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be
10   obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

15   It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical
20   carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

The nucleic acid molecules of the invention can be inserted into vectors and used as
25   gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (*see, e.g.*, U.S. Patent No. 5,328,470) or by stereotactic injection (*see, e.g.*, Chen, *et al.*, 1994. *Proc. Natl. Acad. Sci. USA* 91: 3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which
30   the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the

pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack. or dispenser together with instructions for administration.

5   **Screening and Detection Methods**

The isolated nucleic acid molecules of the invention can be used to express NOVX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect NOVX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a NOVX gene, and to modulate NOVX activity, as described further, below. In addition, the

10   NOVX proteins can be used to screen drugs or compounds that modulate the NOVX protein activity or expression as well as to treat disorders characterized by insufficient or excessive production of NOVX protein or production of NOVX protein forms that have decreased or aberrant activity compared to NOVX wild-type protein (*e.g.*; diabetes (regulates insulin release); obesity (binds and transport lipids); metabolic disturbances associated with

15   obesity, the metabolic syndrome X, as well as anorexia and wasting disorders associated with chronic diseases and various cancers, and infectious disease (possesses anti-microbial activity) and the various dyslipidemias. In addition, the anti-NOVX antibodies of the invention can be used to detect and isolate NOVX proteins and modulate NOVX activity. In yet a further aspect, the invention can be used in methods to influence appetite. absorption

20   of nutrients and the disposition of metabolic substrates in both a positive and negative fashion.

The invention further pertains to novel agents identified by the screening assays described herein and uses thereof for treatments as described, *supra*.

Screening Assays

25   The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs) that bind to NOVX proteins or have a stimulatory or inhibitory effect on, *e.g.*, NOVX protein expression or NOVX protein activity. The invention also includes compounds identified in the screening assays

30   described herein.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of the membrane-bound form of a NOVX protein or polypeptide or biologically-active portion thereof. The test compounds of the invention can be obtained using any of the numerous approaches in combinatorial

5   library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are applicable to peptide, non-peptide

10   oligomer or small molecule libraries of compounds. *See, e.g.*, Lam, 1997. *Anticancer Drug Design* 12: 145.

A "small molecule" as used herein, is meant to refer to a composition that has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be, *e.g.*, nucleic acids, peptides, polypeptides, peptidomimetics,

15   carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention.

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt, *et al.*, 1993. *Proc. Natl. Acad. Sci. U.S.A.* 90: 6909; Erb, *et al.*,

20   1994. *Proc. Natl. Acad. Sci. U.S.A.* 91: 11422; Zuckermann, *et al.*, 1994. *J. Med. Chem.* 37: 2678; Cho, *et al.*, 1993. *Science* 261: 1303; Carrell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2059; Carell, *et al.*, 1994. *Angew. Chem. Int. Ed. Engl.* 33: 2061; and Gallop, *et al.*, 1994. *J. Med. Chem.* 37: 1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992.

25   *Biotechniques* 13: 412-421), or on beads (Lam, 1991. *Nature* 354: 82-84), on chips (Fodor, 1993. *Nature* 364: 555-556), bacteria (Ladner, U.S. Patent No. 5,223,409), spores (Ladner, U.S. Patent 5,233,409), plasmids (Cull, *et al.*, 1992. *Proc. Natl. Acad. Sci. USA* 89: 1865-1869) or on phage (Scott and Smith, 1990. *Science* 249: 386-390; Devlin, 1990. *Science* 249: 404-406; Cwirla, *et al.*, 1990. *Proc. Natl. Acad. Sci. U.S.A.* 87: 6378-6382;

30   Felici, 1991. *J. Mol. Biol.* 222: 301-310; Ladner, U.S. Patent No. 5,233,409.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the

cell surface is contacted with a test compound and the ability of the test compound to bind to a NOVX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the NOVX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic

5   label such that binding of the test compound to the NOVX protein or biologically-active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I, ^{35}S, ^{14}C, or ^{3}H, either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically-labeled with, for

10   example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a known compound which binds NOVX to form an assay mixture, contacting the assay

15   mixture with a test compound, and determining the ability of the test compound to interact with a NOVX protein, wherein determining the ability of the test compound to interact with a NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX protein or a biologically-active portion thereof as compared to the known compound.

20   In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of NOVX protein, or a biologically-active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (e.g., stimulate or inhibit) the activity of the NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to

25   modulate the activity of NOVX or a biologically-active portion thereof can be accomplished, for example, by determining the ability of the NOVX protein to bind to or interact with a NOVX target molecule. As used herein, a "target molecule" is a molecule with which a NOVX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a NOVX interacting protein, a molecule on the surface of

30   a second cell, a molecule in the extracellular milieu, a molecule associated with the internal surface of a cell membrane or a cytoplasmic molecule. A NOVX target molecule can be a non-NOVX molecule or a NOVX protein or polypeptide of the invention. In one embodiment, a NOVX target molecule is a component of a signal transduction pathway that

facilitates transduction of an extracellular signal (*e.g.* a signal generated by binding of a compound to a membrane-bound NOVX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with NOVX.

5   Determining the ability of the NOVX protein to bind to or interact with a NOVX target molecule can be accomplished by one of the methods described above for determining direct binding. In one embodiment, determining the ability of the NOVX protein to bind to or interact with a NOVX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target
10   molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+}, diacylglycerol, IP_3, *etc.*), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the induction of a reporter gene (comprising a NOVX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell
15   survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the invention is a cell-free assay comprising contacting a NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to bind to the NOVX protein or biologically-active portion thereof. Binding of the test compound to the NOVX protein can
20   be determined either directly or indirectly as described above. In one such embodiment, the assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a NOVX protein, wherein determining the ability of the test compound to interact with
25   a NOVX protein comprises determining the ability of the test compound to preferentially bind to NOVX or biologically-active portion thereof as compared to the known compound.

In still another embodiment, an assay is a cell-free assay comprising contacting NOVX protein or biologically-active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.* stimulate or inhibit) the activity of the
30   NOVX protein or biologically-active portion thereof. Determining the ability of the test compound to modulate the activity of NOVX can be accomplished, for example, by determining the ability of the NOVX protein to bind to a NOVX target molecule by one of

the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of NOVX protein can be accomplished by determining the ability of the NOVX protein further modulate a NOVX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an

5   appropriate substrate can be determined as described, *supra*.

In yet another embodiment, the cell-free assay comprises contacting the NOVX protein or biologically-active portion thereof with a known compound which binds NOVX protein to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a NOVX protein, wherein

10   determining the ability of the test compound to interact with a NOVX protein comprises determining the ability of the NOVX protein to preferentially bind to or modulate the activity of a NOVX target molecule.

The cell-free assays of the invention are amenable to use of both the soluble form or the membrane-bound form of NOVX protein. In the case of cell-free assays comprising the

15   membrane-bound form of NOVX protein, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of NOVX protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton$^\circledR$ X-100, Triton$^\circledR$ X-114, Thesit$^\circledR$,

20   Isotridecypoly(ethylene glycol ether)$_n$, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the invention, it may be desirable to immobilize either NOVX protein or its target molecule to facilitate

25   separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to NOVX protein, or interaction of NOVX protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and

30   micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-NOVX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione

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sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter

plates, that are then combined with the test compound or the test compound and either the

non-adsorbed target protein or NOVX protein, and the mixture is incubated under

conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and

5   pH). Following incubation, the beads or microtiter plate wells are washed to remove any

unbound components, the matrix immobilized in the case of beads, complex determined

either directly or indirectly, for example, as described, *supra*. Alternatively, the complexes

can be dissociated from the matrix, and the level of NOVX protein binding or activity

determined using standard techniques.

10   Other techniques for immobilizing proteins on matrices can also be used in the

screening assays of the invention. For example, either the NOVX protein or its target

molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated

NOVX protein or target molecules can be prepared from biotin-NHS

(N-hydroxy-succinimide) using techniques well-known within the art (*e.g.*, biotinylation kit,

15   Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96

well plates (Pierce Chemical). Alternatively, antibodies reactive with NOVX protein or

target molecules, but which do not interfere with binding of the NOVX protein to its target

molecule, can be derivatized to the wells of the plate, and unbound target or NOVX protein

trapped in the wells by antibody conjugation. Methods for detecting such complexes, in

20   addition to those described above for the GST-immobilized complexes, include

immunodetection of complexes using antibodies reactive with the NOVX protein or target

molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity

associated with the NOVX protein or target molecule.

In another embodiment, modulators of NOVX protein expression are identified in a

25   method wherein a cell is contacted with a candidate compound and the expression of

NOVX mRNA or protein in the cell is determined. The level of expression of NOVX

mRNA or protein in the presence of the candidate compound is compared to the level of

expression of NOVX mRNA or protein in the absence of the candidate compound. The

candidate compound can then be identified as a modulator of NOVX mRNA or protein

30   expression based upon this comparison. For example, when expression of NOVX mRNA

or protein is greater (*i.e.*, statistically significantly greater) in the presence of the candidate

compound than in its absence, the candidate compound is identified as a stimulator of

NOVX mRNA or protein expression. Alternatively, when expression of NOVX mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of NOVX mRNA or protein expression. The level of NOVX mRNA or protein expression in the cells can be

5   determined by methods described herein for detecting NOVX mRNA or protein.

In yet another aspect of the invention, the NOVX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos, et al., 1993. Cell 72: 223-232; Madura, et al., 1993. J. Biol. Chem. 268: 12046-12054; Bartel, et al., 1993. Biotechniques 14: 920-924; Iwabuchi, et al., 1993.

10   Oncogene 8: 1693-1696; and Brent WO 94/10300), to identify other proteins that bind to or interact with NOVX ("NOVX-binding proteins" or "NOVX-bp") and modulate NOVX activity. Such NOVX-binding proteins are also involved in the propagation of signals by the NOVX proteins as, for example, upstream or downstream elements of the NOVX pathway.

15   The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for NOVX is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an

20   unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, in vivo, forming a NOVX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) that is operably linked to a transcriptional

25   regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with NOVX.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. By way of example, and not of limitation, these sequences can be used to: (*i*) map

5   their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (*ii*) identify an individual from a minute biological sample (tissue typing); and (*iii*) aid in forensic identification of a biological sample. Some of these applications are described in the subsections, below.

Chromosome Mapping

10   Once the sequence (or a portion of the sequence) of a gene has been isolated, this sequence can be used to map the location of the gene on a chromosome. This process is called chromosome mapping. Accordingly, portions or fragments of the NOVX sequences of SEQ ID NO:2n-1, wherein n is an integer between 1 and 127, or fragments or derivatives thereof, can be used to map the location of the NOVX genes, respectively, on a

15   chromosome. The mapping of the NOVX sequences to chromosomes is an important first step in correlating these sequences with genes associated with disease.

Briefly, NOVX genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the NOVX sequences. Computer analysis of the NOVX, sequences can be used to rapidly select primers that do not span more than one

20   exon in the genomic DNA, thus complicating the amplification process. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the NOVX sequences will yield an amplified fragment.

Somatic cell hybrids are prepared by fusing somatic cells from different mammals

25   (*e.g.*, human and mouse cells). As hybrids of human and mouse cells grow and divide, they gradually lose human chromosomes in random order, but retain the mouse chromosomes. By using media in which mouse cells cannot grow, because they lack a particular enzyme, but in which human cells can, the one human chromosome that contains the gene encoding the needed enzyme will be retained. By using various media, panels of hybrid cell lines can

30   be established. Each cell line in a panel contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, allowing easy

mapping of individual genes to specific human chromosomes. *See, e.g.,* D'Eustachio, *et al.,* 1983. *Science* 220: 919-924. Somatic cell hybrids containing only fragments of human chromosomes can also be produced by using human chromosomes with translocations and deletions.

5   PCR mapping of somatic cell hybrids is a rapid procedure for assigning a particular sequence to a particular chromosome. Three or more sequences can be assigned per day using a single thermal cycler. Using the NOVX sequences to design oligonucleotide primers, sub-localization can be achieved with panels of fragments from specific chromosomes.

10   Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. Chromosome spreads can be made using cells whose division has been blocked in metaphase by a chemical like colcemid that disrupts the mitotic spindle. The chromosomes can be treated briefly with trypsin, and then stained with Giemsa. A pattern of light and

15   dark bands develops on each chromosome, so that the chromosomes can be identified individually. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases, will suffice to get good results at a

20   reasonable amount of time. For a review of this technique, *see,* Verma, *et al.,* HUMAN CHROMOSOMES: A MANUAL OF BASIC TECHNIQUES (Pergamon Press, New York 1988).

Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to

25   noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. Such

30   data are found, *e.g.,* in McKusick, MENDELIAN INHERITANCE IN MAN, available on-line through Johns Hopkins University Welch Medical Library). The relationship between genes and disease, mapped to the same chromosomal region, can then be identified through

linkage analysis (co-inheritance of physically adjacent genes), described in, *e.g.*, Egeland, *et al.*, 1987. *Nature*, 325: 783-787.

Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the NOVX gene, can be determined. If a mutation
5   is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete
10   sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

The NOVX sequences of the invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with
15   one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Patent No. 5,272,057).

Furthermore, the sequences of the invention can be used to provide an alternative
20   technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the NOVX sequences described herein can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner,
25   can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The NOVX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater
30   degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic

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variation is due to single nucleotide polymorphisms (SNPs), which include restriction
fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard
against which DNA from an individual can be compared for identification purposes.

5   Because greater numbers of polymorphisms occur in the noncoding regions, fewer
sequences are necessary to differentiate individuals. The noncoding sequences can
comfortably provide positive individual identification with a panel of perhaps 10 to 1,000
primers that each yield a noncoding amplified sequence of 100 bases. If coding sequences,
such as those of SEQ ID NO:$2n$-1, wherein n is an integer between 1 and 127, are used, a

10   more appropriate number of primers for positive individual identification would be
500-2,000.

Predictive Medicine

The invention also pertains to the field of predictive medicine in which diagnostic
assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for

15   prognostic (predictive) purposes to thereby treat an individual prophylactically.
Accordingly, one aspect of the invention relates to diagnostic assays for determining NOVX
protein and/or nucleic acid expression as well as NOVX activity, in the context of a
biological sample (e.g., blood, serum, cells, tissue) to thereby determine whether an
individual is afflicted with a disease or disorder, or is at risk of developing a disorder,

20   associated with aberrant NOVX expression or activity. The disorders include metabolic
disorders, diabetes, obesity, infectious disease, anorexia, cancer-associated cachexia, cancer,
neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
and hematopoietic disorders, and the various dyslipidemias, metabolic disturbances
associated with obesity, the metabolic syndrome X and wasting disorders associated with

25   chronic diseases and various cancers. The invention also provides for prognostic (or
predictive) assays for determining whether an individual is at risk of developing a disorder
associated with NOVX protein, nucleic acid expression or activity. For example, mutations
in a NOVX gene can be assayed in a biological sample. Such assays can be used for
prognostic or predictive purpose to thereby prophylactically treat an individual prior to the

30   onset of a disorder characterized by or associated with NOVX protein, nucleic acid
expression, or biological activity.

Another aspect of the invention provides methods for determining NOVX protein, nucleic acid expression or activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or

5   prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of NOVX in clinical trials.

10   These and other agents are described in further detail in the following sections.

Diagnostic Assays

An exemplary method for detecting the presence or absence of NOVX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting NOVX protein or

15   nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes NOVX protein such that the presence of NOVX is detected in the biological sample. An agent for detecting NOVX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to NOVX mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length NOVX nucleic acid, such as the nucleic acid of SEQ ID NO:2n-1, wherein n is an integer between 1

20   and 127, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to NOVX mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays of the invention are described herein.

An agent for detecting NOVX protein is an antibody capable of binding to NOVX

25   protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')$_2$) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or

30   antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary

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antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect

5   NOVX mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of NOVX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of NOVX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of

10   NOVX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of NOVX protein include introducing into a subject a labeled anti-NOVX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test

15   subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent

20   capable of detecting NOVX protein, mRNA, or genomic DNA, such that the presence of NOVX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of NOVX protein, mRNA or genomic DNA in the control sample with the presence of NOVX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of NOVX in a

25   biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting NOVX protein or mRNA in a biological sample; means for determining the amount of NOVX in the sample; and means for comparing the amount of NOVX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect NOVX protein or nucleic

30   acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify
subjects having or at risk of developing a disease or disorder associated with aberrant
NOVX expression or activity. For example, the assays described herein, such as the
5   preceding diagnostic assays or the following assays, can be utilized to identify a subject
having or at risk of developing a disorder associated with NOVX protein, nucleic acid
expression or activity. Alternatively, the prognostic assays can be utilized to identify a
subject having or at risk for developing a disease or disorder. Thus, the invention provides
a method for identifying a disease or disorder associated with aberrant NOVX expression or
10   activity in which a test sample is obtained from a subject and NOVX protein or nucleic acid
(*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of NOVX protein or nucleic
acid is diagnostic for a subject having or at risk of developing a disease or disorder
associated with aberrant NOVX expression or activity. As used herein, a "test sample"
refers to a biological sample obtained from a subject of interest. For example, a test sample
15   can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine
whether a subject can be administered an agent (*e.g.*, an agonist, antagonist,
peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to
treat a disease or disorder associated with aberrant NOVX expression or activity. For
20   example, such methods can be used to determine whether a subject can be effectively
treated with an agent for a disorder. Thus, the invention provides methods for determining
whether a subject can be effectively treated with an agent for a disorder associated with
aberrant NOVX expression or activity in which a test sample is obtained and NOVX protein
or nucleic acid is detected (*e.g.*, wherein the presence of NOVX protein or nucleic acid is
25   diagnostic for a subject that can be administered the agent to treat a disorder associated with
aberrant NOVX expression or activity).

The methods of the invention can also be used to detect genetic lesions in a NOVX
gene, thereby determining if a subject with the lesioned gene is at risk for a disorder
characterized by aberrant cell proliferation and/or differentiation. In various embodiments,
30   the methods include detecting, in a sample of cells from the subject, the presence or absence
of a genetic lesion characterized by at least one of an alteration affecting the integrity of a
gene encoding a NOVX-protein, or the misexpression of the NOVX gene. For example,

such genetic lesions can be detected by ascertaining the existence of at least one of: (*i*) a deletion of one or more nucleotides from a NOVX gene; (*ii*) an addition of one or more nucleotides to a NOVX gene; (*iii*) a substitution of one or more nucleotides of a NOVX gene, (*iv*) a chromosomal rearrangement of a NOVX gene; (*v*) an alteration in the level of a

5   messenger RNA transcript of a NOVX gene, (*vi*) aberrant modification of a NOVX gene, such as of the methylation pattern of the genomic DNA, (*vii*) the presence of a non-wild-type splicing pattern of a messenger RNA transcript of a NOVX gene, (*viii*) a non-wild-type level of a NOVX protein, (*ix*) allelic loss of a NOVX gene, and (*x*) inappropriate post-translational modification of a NOVX protein. As described herein,

10 there are a large number of assay techniques known in the art which can be used for detecting lesions in a NOVX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

15   In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (*see, e.g.,* U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (*see, e.g.,* Landegran, *et al.,* 1988. *Science* 241: 1077-1080; and Nakazawa, *et al.,* 1994. *Proc. Natl. Acad. Sci. USA* 91: 360-364), the latter of which can be particularly useful for

20 detecting point mutations in the NOVX-gene (*see,* Abravaya, *et al.,* 1995. *Nucl. Acids Res.* 23: 675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.,* genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a NOVX gene under conditions such that hybridization and amplification of the NOVX gene

25 (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

30   Alternative amplification methods include: self sustained sequence replication (*see,* Guatelli, *et al.,* 1990. *Proc. Natl. Acad. Sci. USA* 87: 1874-1878), transcriptional amplification system (*see,* Kwoh, *et al.,* 1989. *Proc. Natl. Acad. Sci. USA* 86: 1173-1177);

Qβ Replicase (*see*, Lizardi, *et al*, 1988. *BioTechnology* 6: 1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low

5   numbers.

In an alternative embodiment, mutations in a NOVX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and

10   compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (*see, e.g.*, U.S. Patent No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in NOVX can be identified by hybridizing

15   a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes. *See, e.g.*, Cronin, *et al.*, 1996, *Human Mutation* 7: 244-255; Kozal, *et al.*, 1996, *Nat. Med.* 2: 753-759. For example, genetic mutations in NOVX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, *et al., supra.* Briefly, a first hybridization array of

20   probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected.

25   Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the NOVX gene and detect mutations by comparing the sequence of the sample NOVX with the corresponding wild-type (control) sequence.

30   Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert, 1977. *Proc. Natl. Acad. Sci. USA* 74: 560 or Sanger, 1977. *Proc. Natl. Acad. Sci. USA* 74: 5463. It is also contemplated that any of a variety of automated sequencing

procedures can be utilized when performing the diagnostic assays (*see, e.g.,* Naeve, *et al.,* 1995. *Biotechniques* 19: 448), including sequencing by mass spectrometry (*see, e.g.,* PCT International Publication No. WO 94/16101; Cohen, *et al.,* 1996, *Adv. Chromatography* 36: 127-162; and Griffin, *et al.,* 1993. *Appl. Biochem. Biotechnol.* 38: 147-159).

5   Other methods for detecting mutations in the NOVX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes. *See, e.g.,* Myers, *et al.,* 1985. *Science* 230: 1242. In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type NOVX sequence with

10   potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S_1 nuclease to enzymatically digesting the mismatched regions. In other embodiments,

15   either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. *See, e.g.,* Cotton, *et al.,* 1988. *Proc. Natl. Acad. Sci. USA* 85: 4397; Saleeba, *et al.,* 1992. *Methods Enzymol.* 217: 286-295. In

20   an embodiment, the control DNA or RNA can be labeled for detection.

        In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in NOVX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli*

25   cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches. *See, e.g.,* Hsu, *et al.,* 1994. *Carcinogenesis* 15: 1657-1662. According to an exemplary embodiment, a probe based on a NOVX sequence, *e.g.,* a wild-type NOVX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage

30   products, if any, can be detected from electrophoresis protocols or the like. *See, e.g.,* U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in NOVX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids. *See, e.g.,* Orita, *et al.,* 1989. *Proc. Natl. Acad. Sci. USA*: 86: 2766; Cotton,

5   1993. *Mutat. Res.* 285: 125-144; Hayashi, 1992. *Genet. Anal. Tech. Appl.* 9: 73-79. Single-stranded DNA fragments of sample and control NOVX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected

10   with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. *See, e.g.,* Keen, *et al.,* 1991. *Trends Genet.* 7: 5.

15   In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). *See, e.g.,* Myers, *et al.,* 1985. *Nature* 313: 495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of

20   high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. *See, e.g.,* Rosenbaum and Reissner, 1987. *Biophys. Chem.* 265: 12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective

25   primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. *See, e.g.,* Saiki, *et al.,* 1986. *Nature* 324: 163; Saiki, *et al.,* 1989. *Proc. Natl. Acad. Sci. USA* 86: 6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different

30   mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization; *see, e.g.*, Gibbs, *et al.*,

5   1989. *Nucl. Acids Res.* 17: 2437-2448) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (*see, e.g.*, Prossner, 1993. *Tibtech.* 11: 238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. *See, e.g.*, Gasparini, *et al.*, 1992. *Mol. Cell Probes* 6: 1. It is anticipated that in certain embodiments

10 amplification may also be performed using *Taq* ligase for amplification. *See, e.g.*, Barany, 1991. *Proc. Natl. Acad. Sci. USA* 88: 189. In such cases, ligation will occur only if there is a perfect match at the 3'-terminus of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

15   The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a NOVX gene.

20   Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which NOVX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

25   Agents, or modulators that have a stimulatory or inhibitory effect on NOVX activity (*e.g.*, NOVX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders. The disorders include but are not limited to, *e.g.*, those diseases, disorders and conditions listed above, and more particularly include those diseases, disorders, or conditions associated with

30 homologs of a NOVX protein, such as those summarized in Table A.

In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation

5   between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate dosages and therapeutic regimens. Accordingly, the activity of NOVX protein, expression of NOVX

10   nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons.

15   See *e.g.*, Eichelbaum, 1996, *Clin. Exp. Pharmacol. Physiol.*, 23: 983-985; Linder, 1997. *Clin. Chem.*, 43: 254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic

20   conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

25   As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome pregnancy zone protein precursor enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or

30   show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different

among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive

5   standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

10   Thus, the activity of NOVX protein, expression of NOVX nucleic acid, or mutation content of NOVX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness

15   phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a NOVX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring of Effects During Clinical Trials

20   Monitoring the influence of agents (e.g., drugs, compounds) on the expression or activity of NOVX (e.g., the ability to modulate aberrant cell proliferation and/or differentiation) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase NOVX gene expression, protein levels, or upregulate NOVX activity, can

25   be monitored in clinical trails of subjects exhibiting decreased NOVX gene expression, protein levels, or downregulated NOVX activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease NOVX gene expression, protein levels, or downregulate NOVX activity, can be monitored in clinical trails of subjects exhibiting increased NOVX gene expression, protein levels, or upregulated NOVX activity. In such

30   clinical trials, the expression or activity of NOVX and, preferably, other genes that have been implicated in, for example, a cellular proliferation or immune disorder can be used as a "read out" or markers of the immune responsiveness of a particular cell.

By way of example, and not of limitation, genes, including NOVX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates NOVX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for
5 example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of NOVX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity
10 of NOVX or other genes. In this manner, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the
15 effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (*i*) obtaining a pre-administration sample from a subject prior to administration of the agent; (*ii*) detecting the level of expression of a NOVX protein, mRNA, or genomic DNA in the
20 preadministration sample; (*iii*) obtaining one or more post-administration samples from the subject; (*iv*) detecting the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the post-administration samples; (*v*) comparing the level of expression or activity of the NOVX protein, mRNA, or genomic DNA in the pre-administration sample with the NOVX protein, mRNA, or genomic DNA in the post administration sample or
25 samples; and (*vi*) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of NOVX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of NOVX to lower levels than detected, *i.e.*, to decrease the
30 effectiveness of the agent.

Methods of Treatment

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant NOVX expression or activity. The disorders include but are not limited to, *e.g.*, those

5   diseases, disorders and conditions listed above, and more particularly include those diseases, disorders, or conditions associated with homologs of a NOVX protein, such as those summarized in Table A.

These methods of treatment will be discussed more fully, below.

Diseases and Disorders

10   Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to: (*i*) an aforementioned peptide, or analogs,

15   derivatives, fragments or homologs thereof; (*ii*) antibodies to an aforementioned peptide; (*iii*) nucleic acids encoding an aforementioned peptide; (*iv*) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to an aforementioned peptide) that are utilized to "knockout" endogenous function of an aforementioned peptide by homologous

20   recombination (*see, e.g.*, Capecchi, 1989. *Science* 244: 1288-1292); or (*v*) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between an aforementioned peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not

25   suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, an aforementioned peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

30   Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro*

for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of an aforementioned peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis,

5   immunocytochemistry, *etc.*) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, and the like).

Prophylactic Methods

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant NOVX expression or activity, by administering to

10   the subject an agent that modulates NOVX expression or at least one NOVX activity. Subjects at risk for a disease that is caused or contributed to by aberrant NOVX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the NOVX aberrancy, such that a

15   disease or disorder is prevented or, alternatively, delayed in its progression. Depending upon the type of NOVX aberrancy, for example, a NOVX agonist or NOVX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein. The prophylactic methods of the invention are further discussed in the following subsections.

20   ### Therapeutic Methods

Another aspect of the invention pertains to methods of modulating NOVX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of NOVX protein activity associated with the cell. An agent that modulates NOVX protein

25   activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a NOVX protein, a peptide, a NOVX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more NOVX protein activity. Examples of such stimulatory agents include active NOVX protein and a nucleic acid molecule encoding NOVX that has been introduced into the cell. In another

30   embodiment, the agent inhibits one or more NOVX protein activity. Examples of such inhibitory agents include antisense NOVX nucleic acid molecules and anti-NOVX

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antibodies. These modulatory methods can be performed *in vitro* (*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a NOVX protein or nucleic acid

5   molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, up-regulates or down-regulates) NOVX expression or activity. In another embodiment, the method involves administering a NOVX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant NOVX expression or activity.

10   Stimulation of NOVX activity is desirable *in situ*ations in which NOVX is abnormally downregulated and/or in which increased NOVX activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant cell proliferation and/or differentiation (*e.g.*, cancer or immune associated disorders). Another example of such a situation is where the subject has a

15   gestational disease (*e.g.*, preclampsia).

Determination of the Biological Effect of the Therapeutic

In various embodiments of the invention, suitable *in vitro* or *in vivo* assays are performed to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

20   In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly,

25   for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Prophylactic and Therapeutic Uses of the Compositions of the Invention

The NOVX nucleic acids and proteins of the invention are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders. The disorders

30   include but are not limited to, *e.g.*, those diseases, disorders and conditions listed above, and

more particularly include those diseases, disorders, or conditions associated with homologs of a NOVX protein, such as those summarized in Table A.

As an example, a cDNA encoding the NOVX protein of the invention may be useful in gene therapy, and the protein may be useful when administered to a subject in need

5   thereof. By way of non-limiting example, the compositions of the invention will have efficacy for treatment of patients suffering from diseases, disorders, conditions and the like, including but not limited to those listed herein.

Both the novel nucleic acid encoding the NOVX protein, and the NOVX protein of the invention, or fragments thereof, may also be useful in diagnostic applications, wherein

10   the presence or amount of the nucleic acid or the protein are to be assessed. A further use could be as an anti-bacterial molecule (*i.e.,* some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of antibodies, which immunospecifically-bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

15   The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Example A: Polynucleotide and Polypeptide Sequences, and Homology Data

Example 1.

20   The NOV1 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 1A.

Table 1A. NOV1 Sequence Analysis		
	SEQ ID NO: 1	6988 bp
NOV1a,CG108 440-01 DNA Sequence	GAAGAGCAAGAGGCAGGCTCAGCAAATGGTTCAGCCCCAGTCCCCGGTGGCTGTCAGTCAA AGCAAGCCCGGTTGTTATGACAATGGAAAACACTATCAGATAAATCAACAGTGGGAGCGGA CCTACCTAGGTAATGTGTTGGTTTGTACTTGTTATGGAGGAAGCCGAGGTTTTAACTGCGA AAGTAAACCTGAAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTACCGAGTG GGTGACACTTATGAGCGTCCTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGGCTG GGCGAGGGAGAATAAGCTGTACCATCGCAAACCGCTGCCATGAAGGGGGTCAGTCCTACAA GATTGGTGACACCTGGAGGAGACCACATGAGACTGGTGGTTACATGTTAGAGTGTGTGTGT CTTGGTAATGGAAAAGGAGAATGGACCTGCAAGCCCATAGCTGAGAAGTGTTTTGATCATG CTGCTGGGACTTCCTATGTGGTCGGAGAAACGTGGGAGAAGCCCTACCAAGGCTGGATGAT GGTAGATTGTACTTGCCTGGGAGAAGGCAGCGGACGCATCACTTGCACTTCTAGAAATAGA TGCAACGATCAGGACACAAGGACATCCTATAGAATTGGAGACACCTGGAGCAAGAAGGATA ATCGAGGAAACCTGCTCCAGTGCATCTGCACAGGCAACGGCCGAGGAGAGTGGAAGTGTGA

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GAGGCACACCTCTGTGCAGACCACATCGAGCGGATCTGGCCCCTTCACCGATGTTCGTGCA
GCTGTTTACCAACCGCAGCCTCACCCCCAGCCTCCTCCCTATGGCCACTGTGTCACAGACA
GTGGTGTGGTCTACTCTGTGGGGATGCAGTGGTTGAAGACACAAGGAAATAAGCAAATGCT
TTGCACGTGCCTGGGCAACGGAGTCAGCTGCCAAGAGACAGCTGTAACCCAGACTTACGGT
GGCAACTTAAATGGAGAGCCATGTGTCTTACCATTCACCTACAATGGCAGGACGTTCTACT
CCTGCACCACGGAAGGGCGACAGGACGGACATCTTTGGTGCAGCACAACTTCGAATTATGA
GCAGGACCAGAAATACTCTTTCTGCACAGACCACACTGTTTTGGTTCAGACTCAAGGAGGA
AATTCCAATGGTGCCTTGTGCCACTTCCCCTTCCTATACAACAACCACAATTACACTGATT
GCACTTCTGAGGGCAGAAGAGACAACATGAAGTGGTGTGGGACCACACAGAACTATGATGC
CGACCAGAAGTTTGGGTTCTGCCCCATGGCTGCCCACGAGGAAATCTGCACAACCAATGAA
GGGGTCATGTACCGCATTGGAGATCAGTGGGATAAGCAGCATGACATGGGTCACATGATGA
GGTGCACGTGTGTTGGGAATGGTCGTGGGGAATGGACATGCATTGCCTACTCGCAACTTCG
AGATCAGTGCATTGTTGATGACATCACTTACAATGTGAACGACACATTCCACAAGCGTCAT
GAAGAGGGGCACATGCTGAACTGTACATGCTTCGGTCAGGGTCGGGGCAGGTGGAAGTGTG
ATCCCGTCGACCAATGCCAGGATTCAGAGACTGGGACGTTTTATCAAATTGGAGATTCATG
GGAGAAGTATGTGCATGGTGTCAGATACCAGTGCTACTGCTATGGCCGTGGCATTGGGGAG
TGGCATTGCCAACCTTTACAGACCTATCCAAGCTCAAGTGGTCCTGTCGAAGTATTTATCA
CTGAGACTCCGAGTCAGCCCAACTCCCACCCCATCCAGTGGAATGCACCACAGCCATCTCA
CATTTCCAAGTACATTCTCAGGTGGAGACCTAAAAATTCTGTAGGCCGTTGGAAGGAAGCT
ACCATACCAGGCCACTTAAACTCCTACACCATCAAAGGCCTGAAGCCTGGTGTGGTATACG
AGGGCCAGCTCATCAGCATCCAGCAGTACGGCCACCAAGAAGTGACTCGCTTTGACTTCAC
CACCACCAGCACCAGCACACCTGTGACCAGCAACACCGTGACAGGAGAGACGACTCCCTTT
TCTCCTCTTGTGGCCACTTCTGAATCTGTGACCGAAATCACAGCCAGTAGCTTTGTGGTCT
CCTGGGTCTCAGCTTCCGACACCGTGTCGGGATTCCGGGTGGAATATGAGCTGAGTGAGGA
GGGAGATGAGCCACAGTACCTGGATCTTCCAAGCACAGCCACTTCTGTGAACATCCCTGAC
CTGCTTCCTGGCCGAAAATACATTGTAAATGTCTATCAGATATCTGAGGATGGGGAGCAGA
GTTTGATCCTGTCTACTTCACAAACAACAGCGCCTGATGCCCCTCCTGACCCGACTGTGGA
CCAAGTTGATGACACCTCAATTGTTGTTCGCTGGAGCAGACCCCAGGCTCCCATCACAGGG
TACAGAATAGTCTATTCGCCATCAGTAGAAGGTAGCAGCACAGAACTCAACCTTCCTGAAA
CTGCAAACTCCGTCACCCTCAGTGACTTGCAACCTGGTGTTCAGTATAACATCACTATCTA
TGCTGTGGAAGAAAATCAAGAAAGTACACCTGTTGTCATTCAACAAGAAACCACTGGCACC
CCACGCTCAGATACAGTGCCCTCTCCCAGGGACCTGCAGTTTGTGGAAGTGACAGACGTGA
AGGTCACCATCATGTGGACACCGCCTGAGAGTGCAGTGACCGGCTACCGTGTGGATGTGAT
CCCCGTCAACCTGCCTGGCGAGCACGGGCAGAGGCTGCCCATCAGCAGGAACACCTTTGCA
GAAGTCACCGGGCTGTCCCCTGGGGTCACCTATTACTTCAAAGTCTTTGCAGTGAGCCATG
GGAGGGAGAGCAAGCCTCTGACTGCTCAACAGACAACCAAACTGGATGCTCCCACTAACCT
CCAGTTTGTCAATGAAACTGATTCTACTGTCCTGGTGAGATGGACTCCACCTCGGGCCCAG
ATAACAGGATACCGACTGACCGTGGGCCTTACCCGAAGAGGCCAGCCCAGGCAGTACAATG
TGGGTCCCTCTGTCTCCAAGTACCCCCTGAGGAATCTGCAGCCTGCATCTGAGTACACCGT
ATCCCTCGTGGCCATAAAGGGCAACCAAGAGAGCCCCAAAGCCACTGGAGTCTTTACCACA
CTGCAGCCTGGGAGCTCTATTCCACCTTACAACACCGAGGTGACTGAGACCACCATCGTGA
TCACATGGACGCCTGCTCCAAGAATTGGTTTTAAGCTGGGTGTACGACCAAGCCAGGGAGG
AGAGGCACCACGAGAAGTGACTTCAGACTCAGGAAGCATCGTTGTGTCCGGCTTGACTCCA
GGAGTAGAATACGTCTACACCATCCAAGTCCTGAGAGATGGACAGGAAAGAGATGCGCCAA
TTGTAAACAAAGTGGTGACACCATTGTCTCCACCAACAAACTTGCATCTGGAGGCAAACCC
TGACACTGGAGTGCTCACAGTCTCCTGGGAGAGGAGCACCACCCCAGACATTACTGGTTAT
AGAATTACCACAACCCCTACAAACGGCCAGCAGGGAAATTCTTTGGAAGAAGTGGTCCATG
CTGATCAGAGCTCCTGCACTTTTGATAACCTGAGTCCCGGCCTGGAGTACAATGTCAGTGT
TTACACTGTCAAGGATGACAAGGAAAGTGTCCCTATCTCTGATACCATCATCCCAGCTGTT
CCTCCTCCCACTGACCTGCGATTCACCAACATTGGTCCAGACACCATGCGTGTCACCTGGG
CTCCACCCCCATCCATTGATTTAACCAACTTCCTGGTGCGTTACTCACCTGTGAAAAATGA
GGAAGATGTTGCAGAGTTGTCAATTTCTCCTTCAGACAATGCAGTGGTCTTAACAAATCTC
CTGCCTGGTACAGAATATGTAGTGAGTGTCTCCAGTGTCTACGAACAACATGAGAGCACAC
CTCTTAGAGGAAGACAGAAAACAGGTCTTGATTCCCCAACTGGCATTGACTTTTCTGATAT
TACTGCCAACTCTTTTACTGTGCACTGGATTGCTCCTCGAGCCACCATCACTGGCTACAGG
ATCCGCCATCATCCCGAGCACTTCAGTGGGAGACCTCGAGAAGATCGGGTGCCCCACTCTC
GGAATTCCATCACCCTCACCAACCTCACTCCAGGCACAGAGTATGTGGTCAGCATCGTTGC
TCTTAATGGCAGAGAGGAAAGTCCCTTATTGATTGGCCAACAATCAACAGTTTCTGATGTT
CCGAGGGACCTGGAAGTTGTTGCTGCGACCCCCACCAGCCTACTGATCAGCTGGGATGCTC
CTGCTGTCACAGTGAGATATTACAGGATCACTTACGGAGAAACAGGAGGAAATAGCCCTGT
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	ORF Start: ATG at 26 ORF Stop: TAA at 6986
	SEQ ID NO: 2 2320 aa MW at 255732.8kD
NOV1a,CG108 440-01 Protein Sequence	MVQPQSPVAVSQSKPGCYDNGKHYQINQQWERTYLGNVLVCTCYGGSRGFNCESKPEAEET CFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRP HETGGYMLECVCLGNGKGEWTCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGE GSGRITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCERHTSVQTT SSGSGPFTDVRAAVYQPQPHPQPPPYGHCVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGV SCQETAVTQTYGGNLNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQKYSFC TDHTVLVQTQGGNSNGALCHFPFLYNNHNYTDCTSEGRRDNMKWCGTTQNYDADQKFGFCP MAAHEEICTTNEGVMYRIGDQWDKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDI TYNVNDTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQIGDSWEKYVHGVR YQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFITETPSQPNSHPIQWNAPQPSHISKYILRW RPKNSVGRWKEATIPGHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTSTPV TSNTVTGETTPFSPLVATSESVTEITASSFVVSWVSASDTVSGFRVEYELSEEGDEPQYLD LPSTATSVNIPDLLPGRKYIVNVYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIV

	VRWSRPQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYNITIYAVEENQES TPVVIQQETTGTPRSDTVPSPRDLQFVEVTDVKVTIMWTPPESAVTGYRVDVIPVNLPGEH GQRLPISRNTFAEVTGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKLDAPTNLQFVNETDS TVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKYPLRRNLQPASEYTVSLVAIKGN QESPKATGVFTTLQPGSSIPPYNTEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTS DSGSIVVSGLTPGVEYVYTIQVLRDGQERDAPIVNKVVTPLSPPTNLHLEANPDTGVLTVS WERSTTPDITGYRITTTPTNGQQGNSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDDKE SVPISDTIIPAVPPPTDLRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVAELSI SPSDNAVVLTNLLPGTEYVVSVSSVYEQHESTPLRGRQKTGLDSPTGIDFSDITANSFTVH WIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSITLTNLTPGTEYVVSIVALNGREESP LLIGQQSTVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGS KSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNSISV KWLPSSSPVTGYRVTTTPKNGPGPTKTKTAGPDQTEMTIEGLQPTVEYVVSVYAQNPSGES QPLVQTAVTNIDRPKGLAFTDVDVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDG EEDTAELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFTQVTPTSLSAQWT PPNVQLTGYRVRVTPKEKTGPMKEINLAPDSSSVVVSGLMVATKYEVSVYALKDTLTSRPA QGVVTTLENVSPPRRARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKPDV RSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPSNLRFLATTPNSLLVSWQPP RARITGYIIKYEKPGSPPREVVPRPRPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIG RKKTDELPQLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGTSGQQPSVGQ QMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQEALSQTTISWAPFQDTSEYIISCHPVG TDEEPLQFRVPGTSTSATLTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQP TDDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCDSSRWCHDNGVNYKIGE KWDRQGENGQMMSCTCLGNGKGEFKCDPHEATCYDDGKTYHVGEQWQKEYLGAICSCTCFG GQRGWRCDNCRRPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQADREDS RE
	SEQ ID NO: 3 7361 bp
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	ATGCTTTGGAGGCCAGCGGGGCTGGCGCTGTGACAACTGCCGCAGACCTGGGGGTGAACCC
	AGTCCCGAAGGCACTACTGGCCAGTCCTCCTACAACCAGTATTCTCAGAGATACCATCAGAGAA
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	ACCCTGGGAGTTTCCTGAGGGTTTTCTCATAAATGAGGGCTGCACATTGCCTGTTCTGCTT
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ORF Start: at 3		ORF Stop: at 6663
SEQ ID NO: 4	2220 aa	MW at 243994.0kD

NOV1b.CG108 440-02 Protein Sequence	MLRGPGPGLLLLLAVQCLGTAVPSTGASKSKRQAQQMVQPQSPVAVSQSKPGCYDNGKHYQI NQQWERTYLGNALVCTCYGGSRGFNCESKPEAEETCFDKYTGNTYRVGDTYERPKDSMIWD CTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWTCKPIA EKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGRITCTSRNRCNDQDTRTSYRIGD TWSKKDNRGNLLQCICTGNGRGEWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPY GHCVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGVSCQETAVTQTYGGNSNGEPCVLPFTY NGRTFYSCTTEGRQDGHLWCSTTSNYEQDQKYSFCTDHTVLVQTRGGNSNGALCHFPPFLYN NHNYTDCTSEGRRDNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQWDKQH DMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVNDTFHKRHEEGHMLNCTCFGQG RGRWKCDPVDQCQDSETGTFYQIGDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSG PVEVFITETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIPGHLNSYTIKGL KPGVVYEGQLISIQQYGHQEVTRFDFTTTSTSTPVTSNTVTGETTPFSPLVATSESVTEIT ASSFVVSWVSASDTVSGFRVEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRKYIVNVYQI SEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSRPQAPITGYRIVYSPSVEGSST ELNLPETANSVTLSDLQPGVQYNITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQF VEVTDVKVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPISRNTFAEVTGLSPGVTYYFK VFAVSHGRESKPLTAQQTTKLDAPTNLQFVNETDSTVLVRWTPPRAQITGYRLTVGLTRRG QPRQYNVGPSVSKYPLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYNTEV TETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIVVSGLTPGVEYVYTIQVLRDG QERDAPIVNKVVTPLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNS LEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDDKESVPISDTIIPEVPQLTDLSFVDITDS SIGLRWTPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYYTVTGLEPGIDYDISVITLI NGGESAPTTLTQQTAVPPPTDLRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVA ELSISPSDNAVVLTNLLPGTEYVVSVSSVYEQHESTPLRGRQKTGLDSPTGIDFSDITANS FTVHWIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSITLTNLTPGTEYVVSIVALNGR EESPLLIGQQSTVSDVPRDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFT VPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDN

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TNVNCPIECFMPLDVQADREDSRE
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Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 1B.

Table 1B. Comparison of NOV1a against NOV1b.

Protein Sequence	NOV1a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV1b	1..1951 36..1987	1370/1961 (69%) 1496/1961 (75%)

Three polymorphic variants of NOV1b have been identified and are shown in Table 41A

5   Further analysis of the NOV1a protein yielded the following properties shown in Table 1C.

Table 1C. Protein Sequence Properties NOV1a

PSort analysis:	0.8800 probability located in nucleus; 0.1695 probability located in lysosome (lumen); 0.1000 probability located in mitochondrial matrix space; 0.0000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV1a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several

10   homologous proteins shown in Table 1D.

Table 1D. Geneseq Results for NOV1a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV1a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU74674	Human fibronectin protein - *Homo sapiens*, 2324 aa. [WO200187071-A1, 22-NOV-2001]	1..2320 5..2324	2320/2320 (100%) 2320/2320 (100%)	0.0

AAG68182	Fibronectin protein SEQ ID NO:98 - *Homo sapiens*, 2328 aa. [WO200177327-A1, 18-OCT-2001]	1..2320 9..2328	2320/2320 (100%) 2320/2320 (100%)	0.0
AAR92778	Human fibronectin - *Homo sapiens*, 2324 aa. [WO9604304-A1, 15-FEB-1996]	1..2320 5..2324	2318/2320 (99%) 2318/2320 (99%)	0.0
AAP70373	Human fibronectin gene product - *Homo sapiens*, 2327 aa. [EP207751-A, 07-JAN-1987]	1..2320 8..2327	2318/2320 (99%) 2318/2320 (99%)	0.0
AAM38649	Human polypeptide SEQ ID NO 1794 - *Homo sapiens*, 2355 aa. [WO200153312-A1, 26-JUL-2001]	1..2320 36..2355	2316/2320 (99%) 2317/2320 (99%)	0.0

In a BLAST search of public sequence datbases, the NOV1a protein was found to have homology to the proteins shown in the BLASTP data in Table 1E.

Table 1E. Public BLASTP Results for NOV1a				
Protein Accession Number	Protein/Organism/Length	NOV1a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P02751	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG) - *Homo sapiens* (Human), 2386 aa.	1..2320 36..2386	2318/2351 (98%) 2318/2351 (98%)	0.0
FNHU	fibronectin precursor [validated] - human, 2386 aa.	1..2320 36..2386	2318/2351 (98%) 2318/2351 (98%)	0.0
E981236	FN PLASMID PFHDEL1 MATURE PROTEIN FROM PATENT WO9013653 - vectors, 2231 aa.	1..1946 5..2025	1703/2026 (84%) 1765/2026 (87%)	0.0
P07589	Fibronectin (FN) - *Bos taurus* (Bovine), 2265 aa.	1..2183 5..2213	1642/2239 (73%) 1786/2239 (79%)	0.0
P04937	Fibronectin precursor (FN) - *Rattus norvegicus* (Rat), 2477 aa.	1..2114 37..2071	1393/2128 (65%) 1584/2128 (73%)	0.0

PFam analysis predicts that the NOV1a protein contains the domains shown in Table 1F.

Table 1F. Domain Analysis of NOV1a

Pfam Domain	NOV1a Match Region	Identities/ Similarities for the Matched Region	Expect Value
fn1	17..52	19/41 (46%) 35/41 (85%)	7.9e-17
fn1	62..100	21/41 (51%) 39/41 (95%)	3.2e-19
fn1	106..144	21/41 (51%) 36/41 (88%)	1.6e-17
fn1	151..190	23/41 (56%) 37/41 (90%)	4.7e-21
fn1	196..235	26/41 (63%) 38/41 (93%)	4.6e-20
fn1	273..307	14/41 (34%) 31/41 (76%)	8.1e-13
fn2	325..366	27/42 (64%) 42/42 (100%)	8e-35
fn2	385..426	26/42 (62%) 42/42 (100%)	4.3e-37
fn1	435..473	21/41 (51%) 39/41 (95%)	4.4e-20
fn1	483..520	20/41 (49%) 35/41 (85%)	2.3e-16
fn1	526..564	22/41 (54%) 37/41 (90%)	1.7e-18
fn3	573..656	28/87 (32%) 65/87 (75%)	1.7e-12
fn3	685..765	25/85 (29%) 64/85 (75%)	1.7e-14
fn3	776..854	34/84 (40%) 70/84 (83%)	1.9e-25
fn3	872..951	28/86 (33%) 63/86 (73%)	5.5e-22
fn3	962..1040	27/84 (32%) 67/84 (80%)	8.7e-21
fn3	1052..1127	26/86 (30%) 60/86 (70%)	0.0035
fn3	1139..1221	32/87 (37%) 66/87 (76%)	5.9e-19

fn3	1232..1312	27/85 (32%) 69/85 (81%)	1.8e-21
fn3	1323..1402	32/84 (38%) 68/84 (81%)	1.9e-22
fn3	1413..1495	33/86 (38%) 72/86 (84%)	4e-27
fn3	1507..1586	32/85 (38%) 69/85 (81%)	4.3e-21
fn3	1597..1676	29/86 (34%) 63/86 (73%)	2.7e-15
fn3	1687..1766	31/85 (36%) 64/85 (75%)	2.6e-20
fn3	1779..1857	30/84 (36%) 66/84 (79%)	1.6e-21
fn3	1868..1947	31/86 (36%) 69/86 (80%)	1.8e-24
fn3	2038..2115	25/87 (29%) 61/87 (70%)	5.2e-06
fn1	2140..2179	19/41 (46%) 40/41 (98%)	3.1e-20
fn1	2185..2222	21/41 (51%) 37/41 (90%)	9.4e-19
fn1	2229..2264	18/41 (44%) 36/41 (88%)	7.6e-16

Example 2.

The NOV2 clone was analyzed, and the nucleotide and encoded polypeptide
sequences are shown in Table 2A.

Table 2A. NOV2 Sequence Analysis		
	SEQ ID NO: 5	1309 bp
NOV2a, CG122589-01 DNA Sequence	GCCAGGGTTGCCTGCGGGAGCCAGGCGTCCGCTCTCCACACCTTTCACAGCCCCAGCCCTC AGAGCAACCTCAGCCCAGCCCAGCCCAGCTCCAGCTCCAGCTCCAGCCCGGGCCCCATCAT GGCCAAGGACTTTCAAGATATCCAGCAGCTGAGCTCGGAGGAAAATGACCATCCTTTCCAT CAAGGTGAGGGGCCAGGCACTCGCAGGCTGAATCCCAGGAGAGGAAATCCATTTTTGAAAG GGCCACCTCCTGCCCAGCCCCTGGCACAGCGTCTCTGCTCCATGGTCTGCTTCAGTCTGCT TGCCCTGAGCTTCAACATCCTGCTGCTGGTGGTCATCTGTGTGACTGGGTCCCAAAGTGAG GGTCACAGAGGTGCACAGCTGCAAGCCGAGCTGCGGAGCCTGAAGGAAGCTTTCAGCAACT TCTCCTCGAGCACCCTGACGGAGGTCCAGGCAATCAGCACCCACGGAGGCAGCGTGGGTGA CAAGATCACATCCCTAGGAGCCAAGCTGGAGAAACAGCAGCAGGACCTGAAAGCAGATCAC GATGCCCTGCTCTTCCATCTGAAGCACTTCCCCGTGGACCTGCGCTTCGTGGCCTGCCAGA TGGAGCTCCTCCACAGCAACGGCTCCCAAAGGACCTGCTGCCCCGTCAACTGGGTGGAGCA CCAAGGCAGCTGCTACTGGTTCTCTCACTCCGGGAAGGCCTGGGCTGAGGCGGAGAAGTAC TGCCAGCTGGAGAACGCACACCTGGTGGTCATCAACTCCTGGGAGGAGCAGAAATTCATTG TACAACACACGAACCCCTTCAATACCTGGATAGGTCTCACGGACAGTGATGGCTCTTGGAA ATGGGTGGATGGCACAGACTATAGGCACAACTACAAGAACTGGGCTGTCACTCAGCCAGAT

	AATTGGCACGGGCACGAGCTGGGTGGAAGTGAAGACTGTGTTGAAGTCCAGCCGGATGGCC GCTGGAACGATGACTTCTGCCTGCAGGTGTACCGCTGGGTGTGTGAGAAAAGGCGGAATGC CACCGGCGAGGTGGCCTGACCCCAGCACACCTCTGGCTAACCCATACCCCACACCTGCCCA GCTCTGGCTTCTCTGTTGAGGATTTTGAGGAAAGGGAAGAAACACTGAGACAGGGGTATGGG GAAGAGCTGAGCAAAGAGAGAAAGGAGGTAGTTTAAGAGTCCCTGACCCTGGAGGACTGAG ATCCCACCTCCTTCTGTAATTCATTGTAATTATTATAATCGTCAGCCTCTTCAATGGCGTA GGAAAGAAGAAACAAATGCTTGAATCTC
	ORF Start: ATG at 121　　　　　　　　　　　　　ORF Stop: TGA at 1054
	SEQ ID NO: 6　　　311 aa　　　　　　　MW at 35191.1kD
NOV2a, CG122589-01 Protein Sequence	MAKDFQDIQQLSSEENDHPFHQGEGPGTRRLNPRRGNPFLKGPPPAQPLAQRLCSMVCFSL LALSFNILLLVVICVTGSQSEGHRGAQLQAELRSLKEAFSNFSSSTLTEVQAISTHGGSVG DKITSLGAKLEKQQQDLKADHDALLFHLKHFPVDLRFVACQMELLHSNGSQRTCCPVNWVE HQGSCYWFSHSGKAWAEAEKYCQLENAHLVVINSWEEQKFIVQHTNPFNTWIGLTDSDGSW KWVDGTDYRHNYKNWAVTQPDNWHGHELGGSEDCVEVQPDGRWNDDFCLQVYRWVCEKRRN ATGEVA
	SEQ ID NO: 7　　　1112 bp
NOV2b, CG122589-02 DNA Sequence	GCCAGGGTTGCCTGCGGGAGCCAGGCGTCCGCTCTCCACACCTTTCACAGCCCCAGCCCTC AGAGCAACCTCAGCCCAGCCCAGCCCAGCTCCAGCTCCAGCTCCAGCCCGGGCCCCATCAT GGCCAAGGACTTTCAAGATATCCAGCAGCTGAGCTCGGAGGAAAATGACCATCCTTTCCAT CAAGGTGAGGGGCCAGGCACTCGCGGGCTGAATCCCAGGAGAGGAAATCCATTTTTGAAAG GGCCACCTCCTGCCCAGCCCCTGGCACAGCGTCTCTGCTCCATGGTCTGCTTCAGTCTGCT TGCCCTGAGCTTCAACATCCTGCTGCTGGTGGTCATCTGTGTGACTGGGTCCCAAAGTGCA CAGCTGCAAGCCGAGCTGCGGAGCCTGAAGGAAGCTTTCAGCAACTTCTCCTCGAGCACCC TGACGGAGGTTCAGGCAATCAGCACCCACGGAGGCAGCGTGGGTGACAAGATCACATCCCT AGGAGCCAAGCTGGAGAAACAGCAGCAGGACCTGAAAGCAGATCACGATGCCCTGCTCTTC CATCTGAAGCACTTCCCCGTGGACCTGCGCTTCGTGGCCTGCCAGATGGAGCTCCTCCACA GCAACGGCTCCCAAAGGACCTGCTGCCCCGTCAACTGGGTGGAGCACCAAGGCAGCTGCTA CTGGTTCTCTCACTCCGGGAAGGCCTGGGCTGAGGCGGAGAAGTACTGCCTGCTGGAGAAC GCACACCTGGTGGTCATCAACTCCTGGGAGGAGCAGAAATTCATTGTACAACACACGAACC CCTTCAATACCTGGATAGGTCTCACGGACAGTGATGGCTCTTGGAAATGGGTGGATGGCAC AGACTATAGGCACAACTACAAGAACTGGGCTGTCACTCAGCCAGATAATTGGCACGGGCAC GAGCTGGGTGGAAGTGAAGACTGTGTTGAAGTCCAGCCGGATGGCCGCTGGAACGATGACT TCTGCCTGCAGGTGTACCGATGGGTGTGTGAGAAAAGGCGGAATGCCACCGGCGAGGTGGC CTGACCCCAGCACACCTCTGGCTAACCCATACCCCACACCTGCCCAGCTCTGGCTTCTCTG TTGAGGATTTTGAG
	ORF Start: ATG at 121　　　　　　　　　　　　　ORF Stop: TGA at 1039
	SEQ ID NO: 8　　　306 aa　　　　　　　MW at 34540.4kD
NOV2b, CG122589-02 Protein Sequence	MAKDFQDIQQLSSEENDHPFHQGEGPGTRGLNPRRGNPFLKGPPPAQPLAQRLCSMVCFSL LALSFNILLLVVICVTGSQSAQLQAELRSLKEAFSNFSSSTLTEVQAISTHGGSVGDKITS LGAKLEKQQQDLKADHDALLFHLKHFPVDLRFVACQMELLHSNGSQRTCCPVNWVEHQGSC YWFSHSGKAWAEAEKYCLLENAHLVVINSWEEQKFIVQHTNPFNTWIGLTDSDGSWKWVDG TDYRHNYKNWAVTQPDNWHGHELGGSEDCVEVQPDGRWNDDFCLQVYRWVCEKRRNATGEV A
	SEQ ID NO: 9　　　1055 bp
NOV2c, CG122589-03 DNA Sequence	GCCAGGGTTGCCTGCGGGAGCCAGGCGTCCGCTCTCCACACCTTTCACAGCCCCAGCCCTC AGAGCAACCTCAGCCCAGCCCAGCCCAGCTCCAGCTCCAGCTCCAGCCCGGGCCCCATCAT GGCCAAGGACTTTCAAGATATCCAGCAGCTGAGCTCGGAGGAAAATGACCATCCTTTCCAT CAAGGGCCACCTCCTGCCCAGCCCCTGGCACAGCGTCTCTGCTCCATGGTCTGCTTCAGTC TGCTTGCCCTGAGCTTCAACATCCTGCTGCTGGTGGTCATCTGTGTGACTGGGTCCCAAAG TGCACAGCTGCAAGCCGAGCTGCGGAGCCTGAAGGAAGCTTTCAGCAACTTCTCCTCGAGC ACCCTGACGGAGGTCCAGGCAATCAGCACCCACGGAGGCAGCGTGGGTGACAAGATCACAT CCCTAGGAGCCAAGCTGGAGAAACAGCAGCAGGACCTGAAAGCAGATCACGATGCCCTGCT CTTCCATCTGAAGCACTTCCCCGTGGACCTGCGCTTCGTGGCCTGCCAGATGGAGCTCCTC CACAGCAACGGCTCCCAAAGGACCTGCTGCCCCGTCAACTGGGTGGAGCACCAAGGCAGCT GCTACTGGTTCTCTCACTCCGGGAAGGCCTGGGCTGAGGCGGAGAAGTACTGCCAGCTGGA GAACGCACACCTGGTGGTCATCAACTCCTGGGAGGAGCAGAAATTCATTGTACAACACACG

	AACCCCTTCAATACCTGGATAGGTCTCACGGACAGTGATGGCTCTTGGAAATGGGTGGATG GCACAGACTATAGGCACAACTACAAGAACTGGGCTGTCACTCAGCCAGATAATTGGCACGG GCACGAGCTGGGTGGAAGTGAAGACTGTGTTGAAGTCCAGCCGGATGGCCGCTGGAACGAT GACTTCTGCCTGCAGGTGTACCGCTGGGTGTGTGAGAAAAGGCGGAATGCCACCGGCGAGG TGGCCTGACCCCAGCACACCTCTGGCTAACCCATACCCCACACCTGCCCAGCTCTGGCTTC TCTGTTGAGGATTTTGAG
	ORF Start: ATG at 121		ORF Stop: TGA at 982
	SEQ ID NO: 10	287 aa	MW at 32550.1kD
NOV2c, CG122589-03 Protein Sequence	MAKDFQDIQQLSSEENDHPFHQGPPPAQPLAQRLCSMVCFSLLALSFNILLLVVICVTGSQ SAQLQAELRSLKEAFSNFSSSTLTEVQAISTHGGSVGDKITSLGAKLEKQQQDLKADHDAL LFHLKHFPVDLRFVACQMELLHSNGSQRTCCPVNWVEHQGSCYWFSHSGKAWAEAEKYCQL ENAHLVVINSWEEQKFIVQHTNPFNTWIGLTDSDGSWKWVDGTDYRHNYKNWAVTQPDNWH GHELGGSEDCVEVQPDGRWNDDFCLQVYRWVCEKRRNATGEVA

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 2B.

Table 2B. Comparison of NOV2a against NOV2b and NOV2c.		
Protein Sequence	NOV2a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV2b	1..311 1..306	291/311 (93%) 291/311 (93%)
NOV2c	1..311 1..287	274/311 (88%) 274/311 (88%)

Further analysis of the NOV2a protein yielded the following properties shown in Table 2C.

Table 2C. Protein Sequence Properties NOV2a	
PSort analysis:	0.7900 probability located in plasma membrane; 0.7060 probability located in microbody (peroxisome); 0.3000 probability located in Golgi body; 0.2000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	Cleavage site between residues 3 and 4

A search of the NOV2a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 2D.

Table 2D. Geneseq Results for NOV2a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV2a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAW15246	Asialoglycoprotein receptor L-H2 - *Homo sapiens*, 287 aa. [EP773289-A2, 14-MAY- 1997]	1..311 1..287	287/311 (92%) 287/311 (92%)	e-171

AAW15252	Asialoglycoprotein receptor L-H2 cytoplasmic+extracellular domains - Chimeric *Homo sapiens*, 270 aa. [EP773289-A2, 14-MAY-1997]	1..311 1..270	270/311 (86%) 270/311 (86%)	e-159
AAW15251	Asialoglycoprotein receptor L-H2 extracellular domain - Chimeric *Homo sapiens*, 229 aa. [EP773289-A2, 14-MAY-1997]	83..311 1..229	226/229 (98%) 227/229 (98%)	e-140
AAW15245	Asialoglycoprotein receptor H1 - *Homo sapiens*, 291 aa. [EP773289-A2, 14-MAY-1997]	1..301. 1..278	173/301 (57%) 214/301 (70%)	e-103
AAW15250	Asialoglycoprotein receptor H1 cytoplasmic+extracellular domains - Chimeric *Homo sapiens*, 274 aa. [EP773289-A2, 14-MAY-1997]	1..301 1..261	162/301 (53%) 200/301 (65%)	1e-95

In a BLAST search of public sequence datbases, the NOV2a protein was found to have homology to the proteins shown in the BLASTP data in Table 2E.

Table 2E. Public BLASTP Results for NOV2a				
Protein Accession Number	Protein/Organism/Length	NOV2a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P07307	Asialoglycoprotein receptor 2 (Hepatic lectin H2) (ASGP-R) (ASGPR) - *Homo sapiens* (Human), 311 aa.	1..311 1..311	311/311 (100%) 311/311 (100%)	0.0
P24721	Asialoglycoprotein receptor 2 (Hepatic lectin 2) (MHL-2) (ASGP-R) (ASGPR) - *Mus musculus* (Mouse), 301 aa.	1..307 1..300	198/307 (64%) 225/307 (72%)	e-114
LNRT2	hepatic lectin 2 - rat, 301 aa.	1..307 1..300	191/307 (62%) 225/307 (73%)	e-112
P08290	Asialoglycoprotein receptor R2/3 (Hepatic lectin 2/3) (RHL-2) (ASGP-R) (ASGPR) - *Rattus norvegicus* (Rat), 301 aa.	1..307 1..300	189/307 (61%) 223/307 (72%)	e-109

| AAH32130 | Asialoglycoprotein receptor 1 - *Homo sapiens* (Human), 291 aa. | 1..301 1..278 | 173/301 (57%) 213/301 (70%) | e-103 |

PFam analysis predicts that the NOV2a protein contains the domains shown in Table 2F.

Table 2F. Domain Analysis of NOV2a			
Pfam Domain	NOV2a Match Region	Identities/ Similarities for the Matched Region	Expect Value
lectin_c	194..302	51/127 (40%) 99/127 (78%)	9e-50

Example 3.

The NOV3 clone was analyzed, and the nucleotide and encoded polypeptide

5   sequences are shown in Table 3A.

Table 3A. NOV3 Sequence Analysis	
SEQ ID NO: 11	3934 bp
NOV3a, CG133274-01 DNA Sequence	TCCAGTAAGGAGTCGGGGTCTTCCCCAGTTTTCTCAGCCAGGCGGCGGCGGCGACTGGCAA TGTTTGGCCTCAAAAGAAACGCGGTAATCGGACTCAACCTCTACTGTGGGGGGGCCGGCTT GGGGGCCGGCAGCGGCGGCGCCACCCGCCCGGGAGGGCGACTTTTGGCTACGGAGAAGGAG GCCTCGGCCCGGCGAGAGATAGGGGGGAGGGGAGGCCGGCGCGGTGATTGGCGGAAGCGCCG GCGCAAGCCCCCCGTCCACCCTCACGCCAGACTCCCGGAGGGTCGCGCGGCCGCCGCCCAT TGGCGCCGAGGTCCCCGACGTCACCGCGACCCCCGCGAGGCTGCTTTTCTTCGCGCCCACC CGCCGCGCGGCGGCCGCTTGAGGAGATGGAAGCCCCGGCCGCTGACGCCATCATGTCGCCCG AAGAGGAGCTGGACGGGTACGAGCCGGAGCCTCTCGGGAAGCGGCCGGCTGTCCTGCCGCT GCTGGAGTTGGTCGGGGAATCTGGTAATAACACCAGTACGGACGGGTCACTACCCTCGACG CCGCCGCCAGCAGAGGAGGAGGAGGACGAGTTGTACCGGCAGTCGCTGGAGATTATCTCTC GGTACCTTCGGGAGCAGGCCACCGGCGCCAAGGACACAAAGCCAATGGGCAGGTCTGGGGC CACCAGCAGGAAGGCGCTGGAGACCTTACGACGGGTTGGGGATGGCGTGCAGCGCAACCAC GAGACGGTCTTCCAAGGCATGCTTCGGAAACTGGACATCAAAAACGAAGACGATGTGAAAT CGTTGTCTCGAGTGATGATCCATGTTTTCAGCGACGGCGTAACAAACTGGGGCAGGATTGT GACTCTCATTTCTTTTGGTGCCTTTGTGGCTAAACACTTGAAGACCATAAACCAAGAAAGC TGCATCGAACCATTAGCAGAAAGTATCACAGACGTTCTCGTAAGGACAAAACGGGACTGGC TAGTTAAACAAAGAGGCTGGGATGGGTTTGTGGAGTTCTTCCATGTAGAGGACCTAGAAGG TGGCATCAGGAATGTGCTGCTGGCTTTTGCAGGTGTTGCTGGAGTAGGAGCTGGTTTGGCA TATCTAATAAGATAGCCTTACTGTAAGTGCAATAGTTGACTTTTAACCAACCACCACCACC ACCAAAACCAGTTTATGCAGTTGGACTCCAAGCTGTAACTTCCTAGAGTTGCACCCTAGCA ACCTAGCCAGAAAAGCAAGTGGCAAGAGGATTATGGCTAACAAGAATAAATACATGGGAAG AGTGCTCCCCATTGATTGAAGAGTCACTGTCTGAAAGAAGCAAAGTTCAGTTTCAGCAACA AACAAACTTTGTTTGGGAAGCTATGGAGGAGGACTTTTTAGATTTAGTGAAGATGGTAGGGT GGAAAGACTTAATTTCCTTGTTGAGAACAGGAAAGTGGCCAGTAGCCAGGCAAGTCATAGA ATTGATTACCCGCCGAATTCATTAATTTACTGTAGTAGTGTTAAGAGAAGCACTAAGAATG CCAGTGACCTGTGTAAAAGTTACAAGTAATAGAACTATGACTGTAAGCCTCAGTACTGTAC AAGGGAAGCTTTTCCTCTCTCTAATTAGCTTTCCCAGTATACTTCTTAGAAAGTCCAAGTG TTCAGGACTTTTATACCTGTTATACTTTGGCTTGGTTCCATGATTCTTACTTTATTAGCCT AGTTTATCACCAATAATACTTGACGGAAGGCTCAGTAATTAGTTATGAATATGGATATCCT CAATTCTTAAGACAGCTTGTAAATGTATTTGTAAAAATTGTATATATTTTTACAGAAAGTC TATTTCCTTGAAACGAAGGAAGTATCGAATTTACATTAGTTTTTTTTCATACCCTTTTGAAC TTTGCAACTTCCGTAATTAGGAACCTGTTTCTTACAGCTTTTCTATGCTAAACTTTGTTCT

GTTCAGTTCTAGAGTGTATACAGAACGAATTGATGTGTAACTGTATGCAGACTGGTTGTAG
TGGAACAAATCTGATAACTATGCAGGTTTAAATTTTCTTATCTGATTTTGGTAAGTATTCC
TTAGATAGGTTTTCTTTGAAAACCTGGGATTGAGAGGTTGATGAATGGAAATTCTTTCACT
TCATTATATGCAAGTTTTCAATAATTAGGTCTAAGTGGAGTTTTAAGGTTACTGATGACTT
ACAAATAATGGGCTCTGATTGGGCAATACTCATTTGAGTTCCTTCCATTTGACCTAATTTA
ACTGGTGAAATTTAAAGTGAATTCATGGGCTCATCTTTAAAGCTTTTACTAAAAGATTTTC
AGCTGAATGGAACTCATTAGCTGTGTGCATATAAAAAGATCACATCAGGTGGATGGAGAGA
CATTTGATCCCTTGTTTGCTTAATAAATTATAAAATGATGGCTTGGAAAAGCAGGCTAGTC
TAACCATGGTGCTATTATTAGGCTTGCTTGTTACACACACAGGTCTAAGCCTAGTATGTCA
ATAAAGCAAATACTTACTGTTTTGTTTCTATTAATGATTCCCAAACCTTGTTGCAAGTTTT
TGCATTGGCATCTTTGGATTTCAGTCTTGATGTTTGTTCTATCAGACTTAACCTTTTATTT
CCTGTCCTTCCTTGAAATTGCTGATTGTTCTGCTCCCTCTACAGATATTTATATCAATTCC
TACAGCTTTCCCCTGCCATCCCTGAACTCTTTCTAGCCCTTTTAGATTTTGGCACTGTGAA
ACCCCTGCTGGAAACCTGAGTGACCCTCCCTCCCCAAGAGTCCACAGACCTTTCATCT
TCACGAACTTGATCCTGTTAGCAGGTGGTAATACCATGGGTGCTGTGACACTAACAGTCA
TTGAGAGGTGGGAGGAAGTCCCTTTTCCTTGGACTGGTATCTTTTCAACTATTGTTTTATC
CTGTCTTTGGGGGCAATGTGTCAAAAGTCCCCTCAGGAATTTTCAGAGGAAAGAACATTTT
ATGAGGCTTTCTCTAAAGTTTCCTTTGTATAGGAGTATGCTCACTTAAATTTACAGAAAGA
GGTGAGCTGTGTTAAACCTCAGAGTTTAAAAGCTACTGATAAACTGAAGAAAGTGTCTATA
TTGGAACTAGGGTCATTTGAAAGCTTCAGTCTCGGAACATGACCTTTAGTCTGTGGACTCC
ATTTAAAAATAGGTATGAATAAGATGACTAAGAATGTAATGGGGAAGAACTGCCCTGCCTG
CCCATCTCAGAGCCATAAGGTCATCTTTGCTAGAGCTATTTTTACCTATGTATTTATCGTT
CTTGATCATAAGCCGCTTATTTATATCATGTATCTCTAAGGACCTAAAAGCACTTTATGTA
GTTTTTAATTAATCTTAAGATCTGGTTACGGTAACTAAAAGCCTGTCTGCCAAATCCAGTG
GAAACAAGTGCATAGATGTGAATTGGTTTTTAGGGGCCCCACTTCCCAATTCATTAGGTAT
GACTGTGGAAATACAGACAAGGACTTAGTTGATATTTTGGGCTTGGGGCAGTGAGGGCTTA
GGACACCCCAAGTGGTTTGGGAAAGGAGGGAGGGGAGGTGGTGGGTTTATAGGGGGAGGAGG
CAGGTGGTCTAAGTGCTGACTGGCTACGTAGTTCGGGCAAATCCTCCAAAAGGGAAAGGGA
GGATTTGCTTAGAAGGATGGGGCTCCCAGTGACTACTTTTTGACTTCTGTTTGTCTTACGC
TTCTCTCAGGGAAAAACATGCAGTCCTCTAGTGTTTCATGTACATTCTGTGGGGGGTGAAC
ACCTTGGTTCTGGTTAAACAGCTGTACTTTTGATAGCTGTGCCAGGAAGGGTTAGGACCAA
CTACAAATTAATGTTGGTTGTCAAATGTAGTGTGTTTCCCTAACTTTCTGTTTTTCCTGAG
AAAAAAAAATAAATCTTTTATTCAAATAAA

ORF Start: ATG at 61		ORF Stop: TAG at 1111
SEQ ID NO: 12	350 aa	MW at 37364.9kD

NOV3a, CG133274-01 Protein Sequence	MFGLKRNAVIGLNLYCGGAGLGAGSGGATRPGGRLLATEKEASARREIGGGEAGAVIGGSA GASPPSTLTPDSRRVARPPPIGAEVPDVTATPARLLFFAPTRRAAPLEEMEAPAADAIMSP EEELDGYEPEPLGKRPAVLPLLELVGESGNNTSTDGSLPSTPPPAEEEEDELYRQSLEIIS RYLREQATGAKDTKPMGRSGATSRKALETLRRVGDGVQRNHETVFQGMLRKLDIKNEDDVK SLSRVMIHVFSDGVTNWGRIVTLISFGAFVAKHLKTINQESCIEPLAESITDVLVRTKRDW LVKQRGWDGFVEFFHVEDLEGGIRNVLLAFAGVAGVGAGLAYLIR

SEQ ID NO: 13	724 bp	

NOV3b, CG133274-02 DNA Sequence	ATGTTTGGCCTCAAAAGAAACGCGGTAATCGGACTCAACCTCTACTGTGGGGGGGCCGGCT TGGGGGCCGGCAGCGGCGGCGCCACCCGCCCGGGAGGGCGACTTTTGGCTACGGAGAAGGA GGCCTCGGCCCGGCGAGAGATAGGGGGAGGGGAGGCCGGCGCGGTGATTGGCGCCAAGGAC ACAAAGCCAATGGGCAGGTCTGGGGCCACCAGCAGGAAGGCGCTGGAGACCTTACGACGGG TTGGGGATGGCGTGCAGCGCAACCAGACGGCCTTCCAAGGCATGCTTCGGAAACTGGA CATCAAAAACGAAGACGATGTGAAATCGTTGTCTCGAGTGATGATCCATGTTTTCAGCGAC GGCGTAACAAACTGGGGCAGGATTGTGACTCTCATTTCTTTTGGTGCCTTTGTGGCTAAAC ACTTGAAGACCATAAACCAAGAAAGCTGCATCGAACCATTAGCAGAAAGTATCACAGACGT TCTCGTAAGGACAAAACGGGACTGGCTAGTTAAACAAAGAGGCTGGGATGGGTTTGTGGAG TTCTTCCATGTAGAGGACCTAGAAGGTGGCATCAGGAATGTGCTGCTGGCTTTTGCAGGTG TTGCTGGAGTAGGAGCTGGTTTGGCATATCTAATAAGATAGCCTTACTGTAAGTGCGATAG TTGACTTTTAACCAACCACCACCACCACCAAAACCAGTTTATGCAGTTGGACT

ORF Start: ATG at 1		ORF Stop: TAG at 649
SEQ ID NO: 14	216 aa	MW at 23108.3kD

NOV3b,	MFGLKRNAVIGLNLYCGGAGLGAGSGGATRPGGRLLATEKEASARREIGGGEAGAVIGAKD

119

CG133274-02 Protein Sequence	TKPMGRSGATSRKALETLRRVGDGVQRNHETAFQGMLRKLDIKNEDDVKSLSRVMIHVFSD GVTNWGRIVTLISFGAFVAKHLKTINQESCIEPLAESITDVLVRTKRDWLVKQRGWDGFVE FFHVEDLEGGIRNVLLAFAGVAGVGAGLAYLIR
	SEQ ID NO: 15	667 bp
NOV3c, 278876765 DNA Sequence	CACCGGATCCATGTTTGGCCTCAAAAGAAACGCGGTAATCGGACTCAACCTCTACTGTGGG GGGGCCGGCTTGGGGGCCGGCAGCGGCGGCGCCACCCGCCCGGGAGGGCGACTTTTGGCTA CGGAGAAGGAGGCCTCGGCCCGGCGAGAGATAGGGGGAGGGGAGGCCGGCGCGGTGATTGG CGCCAAGGACACAAAGCCAATGGGCAGGTCTGGGGCCACCAGCAGGAAGGCGCTGGAGACC TTACGACGGGTTGGGGATGGCGTGCAGCGCAACCACGAGACGGCCTTCCAAGGCATGCTTC GGAAACTGGACATCAAAAACGAAGACGATGTGAAATCGTTGTCTCGAGTGATGATCCATGT TTTCAGCGACGGCGTAACAAACTGGGGCAGGATTGTGACTCTCATTTCTTTTGGTGCCTTT GTGGCTAAACACTTGAAGACCATAAACCAAGAAAGCTGCATCGAACCATTAGCAGAAAGTA TCACAGACGTTCTCGTAAGGACAAAACGGGACTGGCTAGTTAAACAAAGAGGCTGGGATGG GTTTGTGGAGTTCTTCCATGTAGAGGACCTAGAAGGTGGCATCAGGAATGTGCTGCTGGCT TTTGCAGGTGTTGCTGGAGTAGGAGCTGGTTTGGCATATCTAATAAGAGTCGACGGC
	ORF Start: at 2	ORF Stop: end of sequence
	SEQ ID NO: 16	222 aa	MW at 23624.8kD
NOV3c, 278876765 Protein Sequence	TGSMFGLKRNAVIGLNLYCGGAGLGAGSGGATRPGGRLLATEKEASARREIGGGEAGAVIG AKDTKPMGRSGATSRKALETLRRVGDGVQRNHETAFQGMLRKLDIKNEDDVKSLSRVMIHV FSDGVTNWGRIVTLISFGAFVAKHLKTINQESCIEPLAESITDVLVRTKRDWLVKQRGWDG FVEFFHVEDLEGGIRNVLLAFAGVAGVGAGLAYLIRVDG
	SEQ ID NO: 17	610 bp
NOV3d, 278881214 DNA Sequence	CACCGGATCCGGCTTGGGGGCCGGCAGCGGCGGCGCCACCCGCCCGGGAGGGCGACTTTTG GCTACGGAGAAGGAGGCCTCGGCCCGGCGAGAGATAGGGGGAGGGGAGGCCGGCGCGGTGA TTGGCGCCAAGGACACAAAGCCAATGGGCAGGTCTGGGGCCACCAGCAGGAAGGCGCTGGA GACCTTACGACGGGTTGGGGATGGCGTGCAGCGCAACCACGAGACGGCCTTCCAAGGCATG CTTCGGAAACTGGACATCAAAAACGAAGACGATGTGAAATCGTTGTCTCGAGTGATGATCC ATGTTTTCAGCGACGGCGTAACAAACTGGGGCAGGATTGTGACTCTCATTTCTTTTGGTGC CTTTGTGGCTAAACACTTGAAGACCATAAACCAAGAAAGCTGCATCGAACCATTAGCAGAA AGTATCACAGACGTTCTCGTAAGGACAAAACGGGACTGGCTAGTTAAACAAAGAGGCTGGG ATGGGTTTGTGGAGTTCTTCCATGTAGAGGACCTAGAAGGTGGCATCAGGAATGTGCTGCT GGCTTTTGCAGGTGTTGCTGGAGTAGGAGCTGGTTTGGCATATCTAATAAGAGTCGACGGC
	ORF Start: at 2	ORF Stop: end of sequence
	SEQ ID NO: 18	203 aa	MW at 21645.5kD
NOV3d, 278881214 Protein Sequence	TGSGLGAGSGGATRPGGRLLATEKEASARREIGGGEAGAVIGAKDTKPMGRSGATSRKALE TLRRVGDGVQRNHETAFQGMLRKLDIKNEDDVKSLSRVMIHVFSDGVTNWGRIVTLISFGA FVAKHLKTINQESCIEPLAESITDVLVRTKRDWLVKQRGWDGFVEFFHVEDLEGGIRNVLL AFAGVAGVGAGLAYLIRVDG

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 3B.

Table 3B. Comparison of NOV3a against NOV3b through NOV3d.		
Protein Sequence	NOV3a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV3b	194..350 60..216	140/157 (89%) 140/157 (89%)
NOV3c	194..350 63..219	140/157 (89%) 140/157 (89%)

NOV3d	194..350	140/157 (89%)
	44..200	140/157 (89%)

Further analysis of the NOV3a protein yielded the following properties shown in Table 3C.

Table 3C. Protein Sequence Properties NOV3a	
PSort analysis:	0.7300 probability located in plasma membrane; 0.6400 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen); 0.1000 probability located in outside
SignalP analysis:	Cleavage site between residues 20 and 21

A search of the NOV3a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 3D.

Table 3D. Geneseq Results for NOV3a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV3a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE02462	Human Mcl-1 protein - *Homo sapiens*, 350 aa. [WO200136594-A1, 25-MAY-2001]	1..350 1..350	350/350 (100%) 350/350 (100%)	0.0
AAR68814	Human mcl-1 gene product - *Homo sapiens*, 350 aa. [WO9429330-A, 22-DEC-1994]	1..350 1..350	349/350 (99%) 349/350 (99%)	0.0
ABB57224	Mouse ischaemic condition related protein sequence SEQ ID NO:570 - *Mus musculus*, 331 aa. [WO200188188-A2, 22-NOV-2001]	1..350 1..331	266/350 (76%) 289/350 (82%)	e-144
AAE02463	Human Mcl-1s/deltaTM variant protein - *Homo sapiens*, 271 aa. [WO200136594-A1, 25-MAY-2001]	1..230 1..230	230/230 (100%) 230/230 (100%)	e-129
AAU76554	Murine Bcl-2 polypeptide - Mus sp. 236 aa. [WO200205835-A2, 24-JAN-2002]	193..319 66..199	45/139 (32%) 65/139 (46%)	2e-08

In a BLAST search of public sequence datbases, the NOV3a protein was found to have homology to the proteins shown in the BLASTP data in Table 3E.

Protein Accession Number	Protein/Organism/Length	NOV3a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
A47476	BCL2 homolog MCL1 - human, 350 aa.	1..350 1..350	350/350 (100%) 350/350 (100%)	0.0
Q9UNJ1	Myeloid cell differentiation protein (Myeloid cell leukemia protein 1) (Myeloid cell leukemia sequence 1) (BCL2-related) - *Homo sapiens* (Human), 350 aa.	1..350 1..350	349/350 (99%) 349/350 (99%)	0.0
Q07820	Induced myeloid leukemia cell differentiation protein Mcl-1 - *Homo sapiens* (Human), 350 aa.	1..350 1..350	348/350 (99%) 349/350 (99%)	0.0
Q9Z1P3	Mcl-1 protein - *Rattus norvegicus* (Rat), 330 aa.	1..350 1..330	271/350 (77%) 286/350 (81%)	e-144
P97287	EAT/MCL-1 protein (MCL1) (Myeloid cell leukemia sequence 1) - *Mus musculus* (Mouse), 331 aa.	1..350 1..331	266/350 (76%) 289/350 (82%)	e-144

Table 3E. Public BLASTP Results for NOV3a

PFam analysis predicts that the NOV3a protein contains the domains shown in Table 3F.

Pfam Domain	NOV3a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Bcl-2	213..312	35/108 (32%) 100/108 (93%)	1.3e-46

Table 3F. Domain Analysis of NOV3a

Example 4.

The NOV4 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 4A.

Table 4A. NOV4 Sequence Analysis		
SEQ ID NO: 19	1076 bp	

NOV4a, CG134430-01 DNA Sequence	TCGTGGTGCTTGGGTGGTCGCCACCAAGAAGACTTTGGTGGGGTAGTCTCGGGGCAGCTCA GCGGCCCGCTGTGCCCGTTTCTGGCCTCGCTCGCAGCTTGCACGTCGAGACTCGTAGGCCG CACCGTAGGGCGAGCGTGCGGGTCGCCGCCGCGGCCGCCTCGGGGTCTGGGCCCAGCCGCA GCCTCTTCTACCGCGGCCGGTTGGGAGTCGCCGCGAGATGCAGCCTCCGGGCCCGCCCCCG GCCTATGCCCCCACTAACGGGGACTTCACCTTTGTCTCCTCAGCAGACGCGGAAGATCTCA GTGGTTCAATAGCATCCCCAGATGTCAAATTAAATCTTGGTGGAGATTTTATCAAAGAATC TACAGCTACTACATTTCTGAGACAAAGAGGTTATGGCTGGCTTCTGGAAGTTGAAGATGAT GATCCTGAAGATAACAAGCCACTCTTGGAAGAATTGGACATTGATCTAAAGGATATTTACT ACAAAATCCGATGTGTTTTGATGCCAATGCCATCACTTGGTTTTAATAGACAAGTGGTGAG AGACAATCCTGACTTTTGGGGTCCTCTGGCTGTTGTTCTTTTCTTTTCCATGATATCATTA TATGGACAGTTTAGGGTGGTCTCATGGATTATAACCATTTGGATATTTGGTTCACTAACAA TTTTCTTACTGGCCAGAGTTCTTGGTGGAGAAGTTGCATATGGCCAAGTCCTTGGAGTTAT AGGATATTCATTACTTCCTCTCATTGTAATAGCCCCTGTACTTTTGGTGGTTGGATCATTT GAAGTGGTGTCTACACTTATAAAAGTGAGAAGCACCAGAGGGACAGGACTTCTAGAAGTTA GAATAATATGAAGTAATCAGGAAATATCTATGCCTACAGAAGCAGCAACCGTAAGATAAAC ATTTGTTACACTTAAGAAATTGCTGAGGTTAATACTTTGTTATAATGGATTATAATATTTG ACATTCATAGTGTTGACCCTGGAATCTTTCACAGAAAGCTTGGGGGTCAGGACCAGGAGGT AGAATTTTACAAGGCAATAAATGAAGGTCTTTTAAGATC
	ORF Start: ATG at 221		ORF Stop: TGA at 863
	SEQ ID NO: 20	214 aa	MW at 23585.1kD
NOV4a, CG134430-01 Protein Sequence	MQPPGPPPAYAPTNGDFTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGYG WLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGFNRQVVRDNPDFWGPLAVV LFFSMISLYGQFRVVSWIITIWIFGSLTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAP VLLVVGSFEVVSTLIKVRSTRGTGLLEVRII

One polymorphic variant of NOV4a has been identified and is shown in Table 41B.

Further analysis of the NOV4a protein yielded the following properties shown in Table 4B.

Table 4B. Protein Sequence Properties NOV4a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV4a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several

5   homologous proteins shown in Table 4C.

Table 4C. Geneseq Results for NOV4a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV4a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABB89547	Human polypeptide SEQ ID NO 1923 - *Homo sapiens*, 244 aa. [WO200190304-A2, 29-NOV-2001]	1..200 1..200	199/200 (99%) 200/200 (99%)	e-113

AAM40701	Human polypeptide SEQ ID NO 5632 - *Homo sapiens*, 316 aa. [WO200153312-A1, 26-JUL-2001]	1..200 73..272	199/200 (99%) 200/200 (99%)	e-113
AAM38915	Human polypeptide SEQ ID NO 2060 - *Homo sapiens*, 341 aa. [WO200153312-A1, 26-JUL-2001]	1..200 98..297	199/200 (99%) 200/200 (99%)	e-113
ABB11939	Human secreted protein homolog, SEQ ID NO:2309 - *Homo sapiens*, 274 aa. [WO200157188-A2, 09-AUG-2001]	1..200 31..230	199/200 (99%) 200/200 (99%)	e-113
ABG02475	Novel human diagnostic protein #2466 - *Homo sapiens*, 297 aa. [WO200175067-A2, 11-OCT-2001]	20..108 209..297	82/89 (92%) 85/89 (95%)	2e-42

In a BLAST search of public sequence datbases, the NOV4a protein was found to have homology to the proteins shown in the BLASTP data in Table 4D.

Table 4D. Public BLASTP Results for NOV4a				
Protein Accession Number	Protein/Organism/Length	NOV4a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BSR8	Similar to RIKEN cDNA 2310034L04 gene - *Homo sapiens* (Human), 244 aa.	1..200 1..200	199/200 (99%) 200/200 (99%)	e-112
Q99KZ9	Hypothetical 32.8 kDa protein - *Mus musculus* (Mouse), 289 aa.	26..200 69..245	169/177 (95%) 174/177 (97%)	2e-92
Q9CYG0	2310034L04Rik protein - *Mus musculus* (Mouse), 140 aa.	1..138 1..140	135/140 (96%) 137/140 (97%)	2e-74
Q9U1Y8	Y60A3A.19 protein - *Caenorhabditis elegans*, 255 aa.	29..195 40..206	89/168 (52%) 118/168 (69%)	7e-46
Q9XTX4	T08D2.6 protein - *Caenorhabditis elegans*, 69 aa.	59..112 13..65	33/54 (61%) 40/54 (73%)	2e-11

PFam analysis predicts that the NOV4a protein contains the domains shown in Table 4E.

Table 4E. Domain Analysis of NOV4a			
Pfam Domain	NOV4a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 5.

The NOV5 clone was analyzed, and the nucleotide and encoded polypeptide

sequences are shown in Table 5A.

Table 5A. NOV5 Sequence Analysis			
	SEQ ID NO: 21	1050 bp	
NOV5a, CG137677-01 DNA Sequence	TCCAGGCAACGCTGCGGCTCCGCCCACGTCATGGCGCCCGAGGAGAACGCGGGGACAGAAC TCTGGCTGCAGGGTTTCGAGCGCCGCTTCCTGGCGGCGCGCTCACTGCGCTCCTTCCCCTG GCAGAGCTTAGAGGCAAAGTTAAGAGACTCATCAGATTCTGAGCTGCTGCGGGATATTTTG CAGAAGACTGTGAAGCATCCCGTGTGTGTGAAGCACCCGCCATCAGTCAAGTATGCCCGGT GCTTTCTCTCAGAACTCATCAAAAAGGTCAGTGCTGTCCACACGGAGCCTTTGGACGAGCT GTACGAGGTGCTGGCGGAGACTCTGATGGCCAAGGAGTCCACCCAGGGCCACCGGAGCTAT TTGCTGCCCTCGGGAGGCTCGTTCACACTTTCCGAGATCACAGCCATCATCTCCCATGGTA CTACAGGCCTGGTCACATGGGACGCCACCCTCTACCTTGCAGAATGGGCCATCGAGAACCC AGCAGCCTTCACTAACAGGGGTGTCCTAGAGCTTGGCAGTGGCGCTGGCCTCACAGGCCTG GCCATCTGCAAGATGTGTCGCCCCCAGGCATACATCTTCAGCGACTGTCACAGCCGGGTCC TCGAGCAGCTCCGAGGGAATGTCCTTCTCAATGGCCTCTCATTAGAGGCAGACATCACTGC CAACTTAGACGCCCCAAGGGTGACAGTGGCCCAGCTGGACTGGGACGTAGCGACAGTCCAT CAGCTCTCTGCCTTCCAGCCAGATATTGTCATTGCAGCAGACGTGCTGTATTGCCCAGAAG CCATCGTGTCACTGGTCGGGGTCCTGCGGAGGCTGGCTGCCTGCCGGGAGCACAAGCAGGC TCCTGAGGTCTACCTGGCCTTTACCGTCCGCAACCCAGAGACGTGCCAGCTGTTCACCACC GAGCTAGGTTGGACTGGGATCAGATGGGAAGTGGAAGCTCATCATGACCAGAAACTGTTTC CCTACAGAGAGCACTTGGAGATGGCAATGCTGAACCTCACACTGTAG<u>GACTCACACACGAC</u> <u>TCCAACGGGCTTG</u>		
	ORF Start: ATG at 31		ORF Stop: TAG at 1021
	SEQ ID NO: 22	330 aa	MW at 36826.8kD
NOV5a, CG137677-01 Protein Sequence	MAPEENAGTELWLQGFERRFLAARSLRSFPWQSLEAKLRDSSDSELLRDILQKTVKHPVCV KHPPSVKYARCFLSELIKKVSAVHTEPLDELYEVLAETLMAKESTQGHRSYLLPSGGSFTL SEITAIISHGTTGLVTWDATLYLAEWAIENPAAFTNRGVLELGSGAGLTGLAICKMCRPQA YIFSDCHSRVLEQLRGNVLLNGLSLEADITANLDAPRVTVAQLDWDVATVHQLSAFQPDIV IAADVLYCPEAIVSLVGVLRRLAACREHKQAPEVYLAFTVRNPETCQLFTTELGWTGIRWE VEAHHDQKLFPYREHLEMAMLNLTL		

Further analysis of the NOV5a protein yielded the following properties shown in

Table 5B.

Table 5B. Protein Sequence Properties NOV5a	
PSort analysis:	0.7000 probability located in plasma membrane; 0.3902 probability located in microbody (peroxisome); 0.2000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV5a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 5C.

Table 5C. Geneseq Results for NOV5a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV5a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB36613	Human FLEXHT-35 protein sequence SEQ ID NO:35 - *Homo sapiens*, 330 aa. [WO200070047-A2, 23-NOV-2000]	1..330 1..330	302/330 (91%) 312/330 (94%)	e-174
ABG13115	Novel human diagnostic protein #13106 - *Homo sapiens*, 425 aa. [WO200175067-A2, 11-OCT-2001]	1..297 23..319	274/297 (92%) 284/297 (95%)	e-158
ABG09575	Novel human diagnostic protein #9566 - *Homo sapiens*, 379 aa. [WO200175067-A2, 11-OCT-2001]	1..330 1..379	259/379 (68%) 277/379 (72%)	e-134
ABG13114	Novel human diagnostic protein #13105 - *Homo sapiens*, 490 aa. [WO200175067-A2, 11-OCT-2001]	1..297 1..346	227/346 (65%) 245/346 (70%)	e-113
AAU33207	Novel human secreted protein #3698 - *Homo sapiens*, 352 aa. [WO200179449-A2, 25-OCT-2001]	33..297 8..246	209/266 (78%) 217/266 (81%)	e-108

5   In a BLAST search of public sequence datbases, the NOV5a protein was found to have homology to the proteins shown in the BLASTP data in Table 5D.

Table 5D. Public BLASTP Results for NOV5a				
Protein Accession Number	Protein/Organism/Length	NOV5a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value

Q96G04	Similar to RIKEN cDNA 5730409G15 gene - *Homo sapiens* (Human), 330 aa.	1..330 1..330	302/330 (91%) 312/330 (94%)	e-174
Q96S85	Hypothetical 33.0 kDa protein - *Homo sapiens* (Human), 296 aa.	1..330 1..296	272/330 (82%) 282/330 (85%)	e-152
Q9CS89	5730409G15Rik protein - *Mus musculus* (Mouse), 319 aa (fragment).	1..298 1..297	214/298 (71%) 242/298 (80%)	e-117
BAC05241	CDNA FLJ40819 fis, clone TRACH2010771 - *Homo sapiens* (Human), 153 aa.	1..159 1..125	113/159 (71%) 116/159 (72%)	1e-53
Q9NVL1	CDNA FLJ10661 fis, clone NT2RP2006106 - *Homo sapiens* (Human), 165 aa.	1..114 1..87	79/114 (69%) 83/114 (72%)	4e-33

PFam analysis predicts that the NOV5a protein contains the domains shown in Table 5E.

Table 5E. Domain Analysis of NOV5a			
Pfam Domain	NOV5a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 6.

The NOV6 clone was analyzed, and the nucleotide and encoded polypeptide

5   sequences are shown in Table 6A.

Table 6A. NOV6 Sequence Analysis		
	SEQ ID NO: 23	948 bp
NOV6a, CG137697-01 DNA Sequence	TCCAGGCAACGCTGCGGCTCCGCCCACGTCATGGCGCCCGAGGAGAACGCGGGGACAGAAC TCTGGCTGCAGGGTTTCGAGCGCCGCTTCCTGGCGGCGCGCTCACTGCGCTCCTTCCCCTG GCAGAGCTTAGAGGCAAAGTTAAGAGACTCATCAGATTCTGAGCTGCTGCGGGATATTTTG CAGAAGACTGTGAAGCATCCCGTGTGTGTGAAGCACCCGCCATCAGTCAAGTATGCCCGGT GCTTTCTCTCAGAACTCATCAAAAAGCCCTCGGGAGGCTCGTTCACACTTTCCGAGATCAC AGCCATCATCTCCCATGGTACTACAGGCCTGGTCACATGGGACGCCACCCTCTACCTTGCA GAATGGGCCATCGAGAACCCAGCAGCCTTCACTAACAGGGGTGTCCTAGAGCTTGGCAGTG GCGCTGGCCTCACAGGCCTGGCCATCTGCAAGATGTGTCGCCCCCAGGCATACATCTTCAG CGACTGTCACAGCCGGGTCCTCGAGCAGCTCCGAGGGAATGTCCTTCTCAATGGCCTCTCA TTAGAGGCAGACATCACTGCCAACTTAGACGCCCCAAGGGTGACAGTGGCCCAGCTGGACT GGGACGTAGCGACAGTCCATCAGCTCTCTGCCTTCCAGCCAGATATTGTCATTGCAGCAGA CGTGCTGTATTGCCCAGAAGCCATCGTGTCACTGGTCGGGGTCCTGCGGAGGCTGGCTGCC TGCCGGGAGCACAAGCAGGCTCCTGAGGTCTACCTGGCCTTTACCGTCCGCAACCCAGAGA CGTGCCAGCTGTTCACCACCGAGCTAGGTTGGACTGGGATCAGATGGGAAGTGGAAGCTCA TCATGACCAGAAACTGTTTCCCTACAGAGAGCACTTGGAGATGGCAATGCTGAACCTCACA CTGTAGGACTCACACACGACTCCAACGGGCTTG

	ORF Start: ATG at 31		ORF Stop: TAG at 919
	SEQ ID NO: 24	296 aa	MW at 33013.5kD
NOV6a, CG137697-01 Protein Sequence	MAPEENAGTELWLQGFERRFLAARSLRSFPWQSLEAKLRDSSDSELLRDILQKTVKHPVCV KHPPSVKYARCFLSELIKKPSGGSFTLSEITAIISHGTTGLVTWDATLYLAEWAIENPAAF TNRGVLELGSGAGLTGLAICKMCRPQAYIFSDCHSRVLEQLRGNVLLNGLSLEADITANLD APRVTVAQLDWDVATVHQLSAFQPDIVIAADVLYCPEAIVSLVGVLRRLAACREHKQAPEV YLAFTVRNPETCQLFTTELGWTGIRWEVEAHHDQKLFPYREHLEMAMLNLTL		

Further analysis of the NOV6a protein yielded the following properties shown in Table 6B.

Table 6B. Protein Sequence Properties NOV6a	
PSort analysis:	0.7000 probability located in plasma membrane; 0.4382 probability located in microbody (peroxisome); 0.2000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in mitochondrial inner membrane
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV6a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several

5   homologous proteins shown in Table 6C.

Table 6C. Geneseq Results for NOV6a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV6a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB36613	Human FLEXHT-35 protein sequence SEQ ID NO:35 - *Homo sapiens*, 330 aa. [WO200070047-A2, 23-NOV-2000]	1..296 1..330	271/330 (82%) 281/330 (85%)	e-151
ABG13115	Novel human diagnostic protein #13106 - *Homo sapiens*, 425 aa. [WO200175067-A2, 11-OCT-2001]	1..263 23..319	243/297 (81%) 253/297 (84%)	e-135
ABG09575	Novel human diagnostic protein #9566 - *Homo sapiens*, 379 aa. [WO200175067-A2, 11-OCT-2001]	19..296 89..379	220/299 (73%) 233/299 (77%)	e-114

| ABG13114 | Novel human diagnostic protein #13105 - *Homo sapiens*, 490 aa. [WO200175067-A2, 11-OCT-2001] | 19..263 89..346 | 188/266 (70%) 203/266 (75%) | 7e-94 |
| AAU33207 | Novel human secreted protein #3698 - *Homo sapiens*, 352 aa. [WO200179449-A2, 25-OCT-2001] | 33..263 8..246 | 183/242 (75%) 194/242 (79%) | 9e-92 |

In a BLAST search of public sequence datbases, the NOV6a protein was found to have homology to the proteins shown in the BLASTP data in Table 6D.

Table 6D. Public BLASTP Results for NOV6a				
Protein Accession Number	Protein/Organism/Length	NOV6a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96S85	Hypothetical 33.0 kDa protein - *Homo sapiens* (Human), 296 aa.	1..296 1..296	272/296 (91%) 282/296 (94%)	e-157
Q96G04	Similar to RIKEN cDNA 5730409G15 gene - *Homo sapiens* (Human), 330 aa.	1..296 1..330	271/330 (82%) 281/330 (85%)	e-151
Q9CS89	5730409G15Rik protein - *Mus musculus* (Mouse), 319 aa (fragment).	1..264 1..297	189/298 (63%) 216/298 (72%)	5e-98
BAC05241	CDNA FLJ40819 fis, clone TRACH2010771 - *Homo sapiens* (Human), 153 aa.	1..125 1..125	113/125 (90%) 116/125 (92%)	6e-59
AAH32519	Similar to hypothetical protein FLJ10661 - *Homo sapiens* (Human), 131 aa.	1..70 1..66	51/70 (72%) 58/70 (82%)	7e-20

PFam analysis predicts that the NOV6a protein contains the domains shown in Table 6E.

Table 6E. Domain Analysis of NOV6a			
Pfam Domain	NOV6a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 7.

The NOV7 clone was analyzed, and the nucleotide and encoded polypeptide

sequences are shown in Table 7A.

Table 7A. NOV7 Sequence Analysis			
	SEQ ID NO: 25	1525 bp	
NOV7a, CG137717-01 DNA Sequence	GCGGCCGCCGCAGTGAGCAACGCGGCAACCGGAGCCCGGCGGGCAGCCGGGGAGGCCGGGA CTGAGAGGGGCGAGCCGCTGGTGCTCCCCGGCGGCAGAGGGCCGCGTCGGCCACGGGCCCG GGAGAGACGCGCTCCAGCCGGCCCCAGGATGTAGGCGATCGGCGGCAGCGCTCCTGCAGGC GGCCGGCTCATCATGAAGAAGCACTCGGCCCGGGTGGCCCCGCTCAGCGCCTGCAACAGTC CGGTCCTGACCCTTACCAAAGTGGAAGGGGAGGAGCGCCCCCGGGACTCCCCGGGCCCGGC GGAGGCCCAGGCACCGGCCGGGGTGGAGGCCGGCGGGAGAGCGAGTCGCCGCTGCTGGACG TGCTCCCGGGCGCAACTCAAGAAGATCTTCTGGGGCGTGGCGGTCGTGCTGTGCGTGTGCT CCTCGTGGGCGGGCTCCACGCAGCTCGCCAAGCTGACCTTCAGGAAGTTCGACGCGCCCTT CACCCTCACGTGGTTTGCCACCAACTGGAACTTTTTATTCTTCCCGTTGTACTACGTGGGG CACGTCTGCAAGTCCACAGAGAAGCAGTCTGTGAAGCAGCGATACAGGGAATGCTGTCGAT TTTTTGGAGACAATGGCTTGACTTTGAAGGTGTTTTTTACCAAGGCAGCACCCTTTGGTGT TCTTTGGACACTCACAAACTACCTGTACTTACATGCAATAAAGAAAATAAACACTACGGAT GTCTCCGTGTTGTTCTGCTGCAACAAAGCTTTTGTGTTCTTGCTCTCATGGATCGTTCTCA GGGACAGATTCATGGGAGTGATTGTGGCCGCCATCCTCGCCATCGCTGGCATTGTGATGAT GACCTACGCTGATGGCTTCCACAGCCACTCCGTCATCGGCATCGCACTGGTGGTGGCCTCA GCATCGGTTTTGTTCAAGCTCCTCCTGGGCAGTGCTAAGTTTGGAGAAGCCGCCTTATTTT TGTCCATCTTGGGTGTGTTTAACATCCTCTTCATCACCTGCATTCCTATTATCCTCTACTT TACCAAAGTGGAATACTGGAGCTCTTTTGATGACATTCCATGGGGAAACCTTTGTGGATTT TCAGTTCTTTTATTGGCATTCAATATTGTATTAAATTTTGGAATTGCCGTTACATATCCCA CTCTGATGTCTCTTGGAATCGTCCTCAGCATACCTGTGAATGCAGTGATTGATCACTACAC CAGTCAGATCGTCTTCAATGGGGTCCGGGTCATCGCCATCATCATCATCGGCCTGGGTTTT CTCCTCCTGCTCCTGCCAGAGGAGTGGGATGTCTGGTTGATCAAGCTGCTCACCCGACTCA AAGTGAGGAAGAAGGAGGAGCCTGCAGAGGGCGCTGCCGACCTGAGCTCAGGACCTCAGAG CAAGAACAGAAGAGCCCGGCCTTCCTTCGCCCGCTAACACCACTCCTCTAGAACTCGGTGG TAATGACTGGGAGGTCTATTCCTGCCGGGAGGAACCTCAGTTGGGTAAGGTGTACATACCT
	ORF Start: ATG at 196		ORF Stop: TAA at 1438
	SEQ ID NO: 26	414 aa	MW at 45936.7kD
NOV7a, CG137717-01 Protein Sequence	MKKHSARVAPLSACNSPVLTLTKVEGEERPRDSPGPAEAQAPAGVEAGGRASRRCWTCSRA QLKKIFWGVAVVLCVCSSWAGSTQLAKLTFRKFDAPFTLTWFATNWNFLFFPLYYVGHVCK STEKQSVKQRYRECCRFFGDNGLTLKVFFTKAAPFGVLWTLTNYLYLHAIKKINTTDVSVL FCCNKAFVFLLSWIVLRDRFMGVIVAAILAIAGIVMMTYADGFHSHSVIGIALVVASASVL FKLLLGSAKFGEAALFLSILGVFNILFITCIPIILYFTKVEYWSSFDDIPWGNLCGFSVLL LAFNIVLNFGIAVTYPTLMSLGIVLSIPVNAVIDHYTSQIVFNGVRVIAIIIIGLGFLLLL LPEEWDVWLIKLLTRLKVRKKEEPAEGAADLSSGPQSKNRRARPSFAR

Further analysis of the NOV7a protein yielded the following properties shown in

Table 7B.

Table 7B. Protein Sequence Properties NOV7a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4663 probability located in mitochondrial inner membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV7a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 7C.

Table 7C. Geneseq Results for NOV7a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV7a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
ABG16671	Novel human diagnostic protein #16662 - *Homo sapiens*, 531 aa. [WO200175067-A2, 11-OCT-2001]	5..284 168..492	160/329 (48%) 208/329 (62%)	2e-80
ABB89266	Human polypeptide SEQ ID NO 1642 - *Homo sapiens*, 134 aa. [WO200190304-A2, 29-NOV-2001]	1..134 1..134	134/134 (100%) 134/134 (100%)	1e-76
AAM36449	Peptide #10486 encoded by probe for measuring placental gene expression - *Homo sapiens*, 77 aa. [WO200157272-A2, 09-AUG-2001]	338..414 1..77	77/77 (100%) 77/77 (100%)	5e-37
AAM76340	Human bone marrow expressed probe encoded protein SEQ ID NO: 36646 - *Homo sapiens*, 77 aa. [WO200157276-A2, 09-AUG-2001]	338..414 1..77	77/77 (100%) 77/77 (100%)	5e-37
AAM63526	Human brain expressed single exon probe encoded protein SEQ ID NO: 35631 - *Homo sapiens*, 77 aa. [WO200157275-A2, 09-AUG-2001]	338..414 1..77	77/77 (100%) 77/77 (100%)	5e-37

5   In a BLAST search of public sequence datbases, the NOV7a protein was found to have homology to the proteins shown in the BLASTP data in Table 7D.

Table 7D. Public BLASTP Results for NOV7a

Protein Accession Number	Protein/Organism/Length	NOV7a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
BAC04479	CDNA FLJ37712 fis, clone BRHIP2018369 - *Homo sapiens* (Human), 490 aa.	27..414 96..490	387/395 (97%) 387/395 (97%)	0.0
Q9JJG8	Brain cDNA, clone MNCb-0335 - *Mus musculus* (Mouse), 335 aa.	114..406 26..325	179/300 (59%) 227/300 (75%)	1e-99
Q8T0 m8	GH20388p - *Drosophila melanogaster* (Fruit fly), 578 aa.	94..379 245..536	102/295 (34%) 165/295 (55%)	7e-46
Q95XC7	Hypothetical 37.3 kDa protein - *Caenorhabditis elegans*, 339 aa.	66..368 16..326	110/320 (34%) 170/320 (52%)	5e-39
Q9VDJ2	CG15688 protein - *Drosophila melanogaster* (Fruit fly), 365 aa.	94..211 245..361	47/119 (39%) 70/119 (58%)	2e-17

PFam analysis predicts that the NOV7a protein contains the domains shown in Table 7E.

Table 7E. Domain Analysis of NOV7a			
Pfam Domain	NOV7a Match Region	Identities/ Similarities for the Matched Region	Expect Value
DUF6	78..222	24/147 (16%) 99/147 (67%)	0.053

Example 8.

The NOV8 clone was analyzed, and the nucleotide and encoded polypeptide

5   sequences are shown in Table 8A.

Table 8A. NOV8 Sequence Analysis			
	SEQ ID NO: 27	898 bp	
NOV8a, CG137793-01 DNA Sequence	TAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGT GTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCT CCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGG GAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAG ACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTC AGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCT CCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGT TGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACT GGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTA CTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATA AAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGT		

	TTGCTGTGGACACAGGATTATTTATCTCAACCCAGCAGCAGGTCACATTTCTCTTGAAGAT TAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAAC AACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTG CTACTCAATTGTCAAACACAGCTTGCAATAAAGGGCGATTCCAG

	ORF Start: ATG at 26		ORF Stop: TGA at 797
	SEQ ID NO: 28	257 aa	MW at 29595.6kD
NOV8a, CG137793-01 Protein Sequence	MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSS TKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVV MEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQL DYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFR LLNPHPKPNPKNN		
	SEQ ID NO: 29	757 bp	
NOV8b, CG137793-02 DNA Sequence	TAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGT GTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCT CCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGG GAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAG ACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGCC ATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAA GTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACC TACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTG TAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGAT TCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTG AAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCA AAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGC AATTGCTACTCAATTGTCAAACACA		
	ORF Start: ATG at 26		ORF Stop: TGA at 680
	SEQ ID NO: 30	218 aa	MW at 25079.5kD
NOV8b, CG137793-02 Protein Sequence	MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSS TKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCHGWRNWDVYKVIYYKDGEALKYWYENHNI SITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGL FISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 8B.

Table 8B. Comparison of NOV8a against NOV8b.		
Protein Sequence	NOV8a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV8b	1..246 1..207	207/246 (84%) 207/246 (84%)

Twenty polymorphic variants of NOV8b have been identified and are shown in Table 41C.

5   Further analysis of the NOV8a protein yielded the following properties shown in Table 8C.

Table 8C. Protein Sequence Properties NOV8a

PSort analysis:	0.4600 probability located in plasma membrane; 0.1594 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 26 and 27

A search of the NOV8a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 8D.

Table 8D. Geneseq Results for NOV8a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV8a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAB31584	Amino acid sequence of a human Fc epsilon receptor alpha-chain - *Homo sapiens*, 257 aa. [WO200104310-A1, 18-JAN-2001]	1..257 1..257	257/257 (100%) 257/257 (100%)	e-155
AAB74667	Human immunoglobulin E receptor I alpha subunit protein - *Homo sapiens*, 257 aa. [WO200111010-A2, 15-FEB-2001]	1..257 1..257	257/257 (100%) 257/257 (100%)	e-155
AAY96230	Human Fc receptor, FcepsilonRIa - *Homo sapiens*, 260 aa. [EP1006183-A1, 07-JUN-2000]	1..257 4..260	257/257 (100%) 257/257 (100%)	e-155
AAW61190	The alpha chain of a Fc epsilon receptor - *Homo sapiens*, 257 aa. [WO9823964-A1, 04-JUN-1998]	1..257 1..257	257/257 (100%) 257/257 (100%)	e-155
AAW24066	Alpha subunit of human high affinity receptor for IgE (human FcERI) - *Homo sapiens*, 257 aa. [US5639660-A, 17-JUN-1997]	1..257 1..257	257/257 (100%) 257/257 (100%)	e-155

In a BLAST search of public sequence datbases, the NOV8a protein was found to
have homology to the proteins shown in the BLASTP data in Table 8E.

Table 8E. Public BLASTP Results for NOV8a

Protein Accession Number	Protein/Organism/Length	NOV8a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P12319	High affinity immunoglobulin epsilon receptor alpha-subunit precursor (FcERI) (IgE Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha) - *Homo sapiens* (Human), 257 aa.	1..257 1..257	257/257 (100%) 257/257 (100%)	e-154
AAH15195	Fc IgE, high affinity I, receptor for, alpha polypeptide - *Homo sapiens* (Human), 257 aa.	1..257 1..257	256/257 (99%) 256/257 (99%)	e-154
CAC28464	Sequence 4 from Patent WO0104310 - *Homo sapiens* (Human), 232 aa (fragment).	26..257 1..232	232/232 (100%) 232/232 (100%)	e-139
CAC28471	Sequence 26 from Patent WO0104310 - Cloning vector pINT1, 660 aa.	1..197 1..197	197/197 (100%) 197/197 (100%)	e-117
CAC28468	Sequence 17 from Patent WO0104310 - Cloning vector pINT1, 756 aa (fragment).	1..197 1..197	197/197 (100%) 197/197 (100%)	e-117

PFam analysis predicts that the NOV8a protein contains the domains shown in Table 8F.

Table 8F. Domain Analysis of NOV8a			
Pfam Domain	NOV8a Match Region	Identities/ Similarities for the Matched Region	Expect Value
ig	44..95	19/54 (35%) 37/54 (69%)	1.4e-10
ig	125..178	14/56 (25%) 37/56 (66%)	0.00018

Example 9.

The NOV9 clone was analyzed, and the nucleotide and encoded polypeptide

5   sequences are shown in Table 9A.

Table 9A. NOV9 Sequence Analysis

| SEQ ID NO: 31 | 4330 bp | |

| NOV9a,
CG137873-01
DNA Sequence | TCTAGGAGCCAGCCCCACCCTTAGAAAAGATGTTTTCCATGAGGATCGTCTGCCTGGTCCT
AAGTGTGGTGGGGCACAGCATGGACTGCAGATAGTGGTGAAGGTGACTTTCTAGCTGAAGGA
GGAGGCGTGCGTGGCCCAAGGGGTTGTGGAAAGACATCAATCTGCCTGCAAAGATTCAGACT
GGCCCTTCTGCTCTGATGAAGACTGGAACTACAAATGCCCTTCTGGCTGCAGGATGAAAGG
GTTGATTGATGAAGTCAATCAAGATTTTACAAACAGAATAAATAAGCTCAAAAATTCACTA
TTTGAATATCAGAAGAACAATAAGGATTCTCATTCGTTGACCACTAATATAATGGAAATTT
TGAGAGGCGATTTTTCCTCAGCCAATAACCGTGATAATACCTACAACCGAGTGTCAGAGGA
TCTGAGAAGCAGAATTGAAGTCCTGAAGCGCAAAGTCATAGAAAAAGTACAGCATATCCAG
CTTCTGCAGAAAAATGTTAGAGCTCAGTTGGTTGATATGAAACGACTGGAGGTGGACATTG
ATATTAAGATCCGATCTTGTCGAGGGTCATGCAGTAGGGCTTTAGCTCGTGAAGTAGATCT
GAAGGACTATGAAGATCAGCAGAAGCAACTTGAACAGGTCATTGCCAAAGACTTACTTCCC
TCTAGAGATAGGCAACACTTACCACTGATAAAAATGAAACCAGTTCCAGACTTGGTTCCCG
GAAATTTTAAGAGCCAGCTTCAGAAGGTACCCCCAGAGTGGAAGGCATTAACAGACATGCC
GCAGATGAGAATGGAGTTAGAGAGACCTGGTGGAAATGAGATTACTCGAGGAGGCTCCACC
TCTTATGGAACCGGATCAGAGACGGAAAGCCCCAGGAACCCTAGCAGTGCTGGAAGCTGGA
ACTCTGGGAGCTCTGGACCTGGAAGTACTGGAAACCGAAACCCTGGGAGCTCTGGGACTGG
AGGGACTGCAACCTGGAAACCTGGGAGCTCTGGACCTGGAAGTACTGGAAGCTGGAACTCT
GGGAGCTCTGGAACTGGAAGTACTGGAAACCAAAACCCTGGGAGCCCTAGACCTGGTAGTA
CCGGAACCTGGAATCCTGGCAGCTCTGAACGCGGAAGTGCTGGGCACTGGACCTCTGAGAG
CTCTGTATCTGGTAGTACTGGACAATGGCACTCTGAATCTGGAAGTTTTAGGCCAGATAGC
CCAGGCTCTGGGAACGCGAGGCCTAACAACCCAGACTGGGGCACATTTGAAGAGGTGTCAG
GAAATGTAAGTCCAGGGACAAGGAGAGAGTACCACACAGAAAAACTGGTCACTTCTAAAGG
AGATAAAGAGCTCAGGACTGGTAAAGAGAAGGTCACCTCTGGTAGCACAACCACCACGCGT
CGTTCATGCTCTAAAACCGTTACTAAGACTGTTATTGGTCCTGATGGTCACAAAGAAGTTA
CCAAAGAAGTGGTGACCTCCGAAGATGGTTCTGACTGTCCCGAGGCAATGGATTTAGGCAC
ATTGTCTGGCATAGGTACTCTGGATGGGTTCCGCCATAGGCACCCTGATGAAGCTGCCTTC
TTCGACACTGCCTCAACTGGAAAAACATTCCCAGGTTTCTTCTCACCTATGTTAGGAGAGT
TTGTCAGTGAGACTGAGTCTAGGGGCTCAGAATCTGGCATCTTCACAAATACAAAGGAATC
CAGTTCTCATCACCCTGGGATAGCTGAATTCCCTTCCCGTGGTAAATCTTCAAGTTACAGC
AAACAATTTACTAGTAGCACGAGTTACAACAGAGGAGACTCCACATTTGAAAGCAAGAGCT
ATAAAATGGCAGATGAGGCCGGAAGTGAAGCCGATCATGAAGGAACACATAGCACCAAGAG
AGGCCATGCTAAATCTCGCCCTGTCAGAGGTATCCACACTTCTCCTTTGGGGAAGCCTTCC
CTGTCCCCCTAGACTAAGTTAAATATTTCTGCACAGTGTTCCCATGGCCCCTTGCATTTCC
TTCTTAACTCTCTGTTACACGTCATTGAAACTACACTTTTTTGGTCTGTTTTTGTGCTAGA
CTGTAAGTTCCTTGGGGGGCAGGGCCTTTGTCTGTCTCATCTCTGTATTCCCAAATGCCTAA
CAGTACAGAGCCATGACTCAATAAATACATGTTAAATGGATGAATGAATTCCTCTGAAACT
CTATTTGAGCTTATTTAGTCAAATTCTTTCACTATTCAAAGTGTGTGCTATTAGAATTGTC
ACCCAACTGATTAATCACATTTTTAGTATGTGTCTCAGTTGACATTTAGGTCAGGCTAAAT
ACAAGTTGTGTTAGTATTAAGTGATGCTTAGCTACCTGTACTGGTTACTTGCTATTAGTTT
GTGCAAGTAAAATTCCAAATACATTTGAGGAAAATCCCCTTTGCAATTTGTAGGTATAAAT
AACCGCTTATTTGCATAAGTTCTATCCCACTGTAAGTGCATCCTTTCCCTATGGAGGGAAG
GAAAGGAGGAAGAAAGAAAGGAAGGGAAAGAAACAGTATTTGCCTTATTTAATCTGAGCCG
TGCCTATCTTTGTAAAGTTAAATGAGAATAACTTCTTCCAACCAGCTTAATTTTTTTTTTA
GACTGTGATGATGTCCTCCAAACACATCCTTCAGGTACCCAAAGTGGCATTTTCAATATCA
AGCTACCGGGATCCAGTAAGATTTTTTCTGTTTATTGCGATCAAGAGACCAGTTTGGGAGG
ATGGCTTTTGATCCAGCAAAGAATGGATGGATCACTGAATTTTAACCGGACCTGGCAAGAC
TACAAGAGAGGTTTCGGCAGCCTGAATGACGAGGGGGAAGGAGAATTCTGGCTAGGCAATG
ACTACCTCCACTTACTAACCCAAAGGGGCTCTGTTCTTAGGGTTGAATTAGAGGACTGGGC
TGGGAATGAAGCTTATGCAGAATATCACTTCCGGGTAGGCTCTGAGGCTGAAGGCTATGCC
CTCCAAGTCTCCTCCTATGAAGGCACTGCGGGTGATGCTCTGATTGAGGGTTCCGTAGAGG
AAGGGGCAGAGTACACCTCTCACAACAACATGCAGTTCAGCACCTTTGACAGGGATGCAGA
CCAGTGGGAAGAGAACTGTGCAGAAGTCTATGGGGGAGGCTGGTGGTATAATAACTGCCAA
GCAGCCAATCTCAATGGAATCTACTACCCTGGGGGCTCCTATGACCCAAGGAATAACAGTC
CTTATGAGATTGAGAATGGAGTGGTCTGGGTTTCCTTTAGAGGGGCAGATTATTCCCTCAG
GGCTGTTCGCATGAAAATTAGGCCCCTTGTGACCCAATAGGCTGAAGAAGTGGGAATGGGA
GCACTCTGTCTTCTTTGCTAGAGAAGTGGAGAGAAAATACAAAAGGTAAAGCAGTTGAGAT
TCTCTACAACCTAAAAAATTCCTAGGTGCTATTTTCTTATCCTTTGTACTGTAGCTAAATG
TACCTGAGACATATTAGTCTTTGAAAAATAAAGTTATGTAAGGTTTTTTTTATCTTTAAAT |

	AGCTCTGTGGGTTTTAACATTTTTGTAAAGATATACCAAGGGCCATTCAGTACATCAGGAA
	AGTGGCAGACAGAAGCTTCTCTCTGCAACCTTGAAGACTATTGGTTTGAGAACTTCTCTTC
	CCATACCACCCAAAATCATAATGCCATTGGAAAGCAAAAAGTTGTTTTATCCATTTGATTT
	GAATTGTTTTAAGCCAATATTTTAAGGTAAAACTCACTGAATCTAACCATAGCTGACCTTT
	GTAGTAGAATTTACAACTTATAATTACAATGCACAATTTATAATTACAATATGTATTTATG
	TCTTTTGCTATGGAGCAAATCCAGGAAGGCAAGAGAAACATTCTTTCCTAAATATAAATGA
	AAATCTATCCTTTAAACTCTTCCACTAGACGTTGTAATGCACACTTATTTTTTTCCCAAGG
	AGTAACCAATTTCTTTCTAAAACACATTTAAAATTTTAAAACTATTTATGAATATTAAAAA
	AAGACATAATTCACACATTAATAAACAATCTCCCAAGTATTGATTTAACTTCATTTTTCTA
	ATAATCATAAACTATATTCTGTGACATGCTAATTATTATTAAATGTAAGTCGTTAGTTCGA
	AAGCCTCTCACTAAGTATGATCTATGCTATATTCAAAATTCAACCCATTTACTTTGGTCAA
	TATTTGATCTAAGTTGCATCTTTAATCCTGGTGGTCTTGCCTTCTGATTTTTAATTTGTAT
	CCTTTTCTATTAAGATATATTTGTCATTTTCTCTTGAATATGTATTAAAATATCCCAAGC
	ORF Start: ATG at 30 **ORF Stop: TAG at 1962**
	SEQ ID NO: 32 644 aa MW at 69756.0kD
NOV9a, CG137873-01 Protein Sequence	MFSMRIVCLVLSVVGTAWTADSGEGDFLAEGGGVRGPRVVERHQSACKDSDWPFCSDEDWN YKCPSGCRMKGLIDEVNQDFTNRINKLKNSLFEYQKNNKDSHSLTTNIMEILRGDFSSANN RDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSCRGS CSRALAREVDLKDYEDQQKQLEQVIAKDLLPSRDRQHLPLIKMKPVPDLVPGNFKSQLQKV PPEWKALTDMPQMRMELERPGGNEITRGGSTSYGTGSETESPRNPSSAGSWNSGSSGPGST GNRNPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSE RGSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTRRE YHTEKLVTSKGDKELRTGKEKVTSGSTTTTRRSCSKTVTKTVIGPDGHKEVTKEVVTSEDG SDCPEAMDLGTLSGIGTLDGFRHRHPDEAAFFDTASTGKTFPGFFSPMLGEFVSETESRGS ESGIFTNTKESSSHHPGIAEFPSRGKSSSYSKQFTSSTSYNRGDSTFESKSYKMADEAGSE ADHEGTHSTKRGHAKSRPVRGIHTSPLGKPSLSP
	SEQ ID NO: 33 1515 bp
NOV9b, CG137873-03 DNA Sequence	AATCCTTTCTTTCAGCTGGAGTGTCCTCAGGAGCCAGCCCCACCCTTAGAAAAGATGTTTT CCATGAGGATCGTCTGCCTGGTCCTAAGTGTGGTGGGCACAGCATGGACTGCAGATAGTGG TGAAGGTGACTTTCTAGCTGAAGGAGGAGGCGTGCGTGGCCCAAGGGTTGTGGAAAGACAT CAATCTGCCTGCAAAGATTCAGACTGGCCCTTCTGCTCTGATGAAGACTGGAACTACAAAT GCCCTTCTGGCTGCAGGATGAAAGGGTTGATTGATGAAGTCAATCAAGATTTTACAAACAG AATAAATAAGCTCAAAAATTCACTATTTGAATATCAGAAGAACAATAAGGATTCTCATTCG TTGACCACTAATATAATGGAAATTTTGAGAGGCGATTTTTCCTCAGCCAATAACCGTGATA ATACCTACAACCGAGTGTCAGAGGATCTGAGAAGCAGAATTGAAGTCCTGAAGCGCAAAGT CATAGAAAAAGTACAGCATATCCAGCTTCTGCAAAAAAATGTTAGAGCTCAGTTGGTTGAT ATGAAACGACTGGAGGTGGACATTGATATTAAGATCCGATCTTGTCGAGGGTCATGCAGTA GGGCTTTAGCTCGTGAAGTAGATCTGAAGGACTATGAAGATCAGCAGAAGCAACTTGAACA GGTCATTGCCAAAGACTTACTTCCCTCTAGAGATAGGCAACACTTACCACTGATCAAAATG AAACCAGTTCCAGACTTGGTTCCCGGAAATTTTAAGAGCCAGCTTCAGAAGGTACCCCCAG AGTGGAAGGCATTAACAGACATGCCGCAGATGAGAATGGAGTTAGAGAGACCTGGTGGAAA TGAGATTACTCGAGGAGGCTCCACCTCTTATGGAACCGGATCAGAGACGGAAAGCCCCAGG AACCCTAGCAGTGCTGGAAGCTGGAACTCTGGGAGCTCTGGACCTGGAAGTACTGGAAGCT GGAAGCTGGAAGTACTGGAAACCAAAACCCTGGGAGCCCTAGACCTGGTAGTACCGGAACC TGGAATCCTGGCAGCTCTGAACGCGGAAGTGCTGGGCACTGGACCTCTGAGAGCTCTGTAT CTGGTAGTACTGGACAATGGCACTCTGAATCTGGAAGTTTTAGGCCAGATAGCCCAGGCTC TGGGAACGCGAGGCCTAACAACCCAGACTGGGGCACATTTGAAGAGGTGTCAGGAAATGTA AGTCCAGGGACAAGAGAGAGTACACACAGAAAACTGGTCCTTCTACAAGAGATAAGAGCTC GGACTGGTAAGAGAGGTCACTCTGGTACACAACACACGCGTGTCATCTCTAAACGTACTAG ACGTATGGCCGATGTCCAGAGTACAGAATGGAACCCAATGTCACTCCAGAAGATAGAATTT AGATTAATTAAGGTCCAAGCCGAATGCTAACTCATAAATGTTACCTAAAAATAGAAACTGA TAATCAATTACATAATAATAAAGATAAAGATAAAAAAAAGAATAAAAAAAA
	ORF Start: ATG at 55 **ORF Stop: TAA at 1219**
	SEQ ID NO: 34 388 aa MW at 43094.6kD
NOV9b, CG137873-03	MFSMRIVCLVLSVVGTAWTADSGEGDFLAEGGGVRGPRVVERHQSACKDSDWPFCSDEDWN YKCPSGCRMKGLIDEVNQDFTNRINKLKNSLFEYQKNNKDSHSLTTNIMEILRGDFSSANN RDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSCRGS

Protein Sequence	CSRALAREVDLKDYEDQQKQLEQVIAKDLLPSRDRQHLPLIKMKPVPDLVPGNFKSQLQKV PPEWKALTDMPQMRMELERPGGNEITRGGSTSYGTGSETESPRNPSSAGSWNSGSSGPGST GSWKLEVLETKTLGALDLVVPEPGILAALNAEVLGTGPLRALYLVVLDNGTLNLEVLGQIA QALGTRGLTTQTGAHLKRCQEM

	SEQ ID NO: 35	1734 bp	
NOV9c, CG137873-02 DNA Sequence	AATCCTTTCTTTCAGCTGGAGTGTCCTCAGGAGCCAGCCCCACCCTTAGAAAAGATGTTTT CCATGAGGATCGTCTGCCTGGTCCTAAGTGTGGTGGGCACAGCATGGACTGCAGATAGTGG TGAAGGTGACTTTCTAGCTGAAGGAGGAGGCGTGCGTGGCCCAAGGGTTGTGGAAAGACAT CAATCTGCCTGCAAAGATTCAGACTGGCCCTTCTGCTCTGATGAAGACTGGAACTACAAAT GCCCTTCTGGCTGCAGGATGAAAGGGTTGATTGATGAAGTCAATCAAGATTTTACAAACAG AATAAATAAGCTCAAAAATTCACTATTTGAATATCAGAAGAACAATAAGGATTCTCATTCG TTGACCACTAATATAATGGAAATTTTGAGAGGCGATTTTTCCTCAGCCAATAACCGTGATA ATACCTACAACCGAGTGTCAGAGGATCTGAGAAGCAGAATTGAAGTCCTGAAGCGCAAAGT CATAGAAAAAGTACAGCATATCCAGCTTCTGCAAAAAAATGTTAGAGCTCAGTTGGTTGAT ATGAAACGACTGGAGGTGGACATTGATATTAAGATCCGATCTTGTCGAGGGTCATGCAGTA GGGCTTTAGCTCGTGAAGTAGATCTGAAGGACTATGAAGATCAGCAGAAGCAACTTGAACA GGTCATTGCCAAAGACTTACTTCCCTCTAGAGATAGGCAACACTTACCACTGATCAAAATG AAACCAGTTCCAGACTTGGTTCCCGGAAATTTTAAGAGCCAGCTTCAGAAGGTACCCCCAG AGTGGAAGGCATTAACAGACATGCCGCAGATGAGAATGGAGTTAGAGAGACCTGGTGGAAA TGAGATTACTCGAGGAGGCTCCACTTCTTATGGAACCGGATCAGAGACGGAAAGCCCAAGG AACCCTAGCAGTGCTGGAAGCTGGAACTCTGGGAGCTCTGGACCTGGAAGTACTGGAAGCT GGAACTCTGGGAGCTCTGGAACTGGAAGTACTGGAAACCAAAACCCTGGGAGCCCTAGACC TGGTAGTACCGGAACCTGGAATCCTGGCAGCTCTGAACGCGGAAGTGCTGGGCACTGGACC TCTGAGAGCTCTGTATCTGGTAGTACTGGACAATGGCACTCTGAATCTGGAAGTTTTAGGC CAGATAGCCCAGGCTCTGGGAACGCGAGGCCTAACAACCCAGACTGGGGCTCAGAATCTGG CATCTTCACAAATACAAAGGAATCCAGTTCTCATCACCCTGGGATAGCTGAATTCCCTTCC CGTGGTAAATCTTCAAGTTACAGCAAACAATTTACTAGTAGCACGAGTTACAACAGAGGAG ACTCCACATTTGAAAGCAAGAGCTATAAAATGGCAGATGAGGCCGGAAGTGAAGCCGATCA TGAAGGAACACATAGCACCAAGAGAGGGCCATGCTAAATCTCGCCCTGTCAGAGGTATCCAC ACTTCTCCTTTGGGGAAGCCTTCCCTGTCCCCCTAGACTAAGTTAAATATTTCTGCACAGT GTTCCCATGGCCCCTTGCATTTCCTTCTTAACTCTCTGTTACACGTCATTGAAACTACACT TTTTTGGTCTGTTTTTGTGCTAGACTGTAAGTTCCTTGGGGGCAGGGCCTTTGTCTGTCTC ATCTCTGTATTCCCAAATGCCTAACAGTACAGGCCCATGACTCAATAAATACATGTTAAAT GGATGAATGAATTCCTCTGAAACTCT

	ORF Start: ATG at 55		ORF Stop: TAG at 1498
	SEQ ID NO: 36	481 aa	MW at 52648.5kD
NOV9c, CG137873-02 Protein Sequence	MFSMRIVCLVLSVVGTAWTADSGEGDFLAEGGGVRGPRVVERHQSACKDSDWPFCSDEDWN YKCPSGCRMKGLIDEVNQDFTNRINKLKNSLFEYQKNNKDSHSLTTNIMEILRGDFSSANN RDNTYNRVSEDLRSRIEVLKRKVIEKVQHIQLLQKNVRAQLVDMKRLEVDIDIKIRSCRGS CSRALAREVDLKDYEDQQKQLEQVIAKDLLPSRDRQHLPLIKMKPVPDLVPGNFKSQLQKV PPEWKALTDMPQMRMELERPGGNEITRGGSTSYGTGSETESPRNPSSAGSWNSGSSGPGST GSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSERGSAGHWTSESSVSGSTGQWHSESGS FRPDSPGSGNARPNNPDWGSESGIFTNTKESSSHHPGIAEFPSRGKSSSYSKQFTSSTSYN RGDSTFESKSYKMADEAGSEADHEGTHSTKRGHAKSRPVRGIHTSPLGKPSLSP

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 9B.

Table 9B. Comparison of NOV9a against NOV9b and NOV9c.		
Protein Sequence	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV9b	1..289 1..289	260/289 (89%) 260/289 (89%)

| NOV9c | 1..412 | 318/412 (77%) |
| | 1..386 | 319/412 (77%) |

Further analysis of the NOV9a protein yielded the following properties shown in Table 9C.

Table 9C. Protein Sequence Properties NOV9a	
PSort analysis:	0.5087 probability located in outside; 0.1900 probability located in lysosome (lumen); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 20 and 21

A search of the NOV9a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several

5 homologous proteins shown in Table 9D.

Table 9D. Geneseq Results for NOV9a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR82244	Human fibrinogen A-alpha chain protein - *Homo sapiens*, 644 aa. [WO9523868-A1, 08-SEP-1995]	1..644 1..644	643/644 (99%) 643/644 (99%)	0.0
AAR60020	Fibronectin - *Homo sapiens*, 643 aa. [WO9416085-A, 21-JUL-1994]	1..644 1..643	641/644 (99%) 641/644 (99%)	0.0
AAY82891	AlphaE subunit of human fibrinogen - *Homo sapiens*, 847 aa. [WO200009562-A1, 24-FEB-2000]	20..641 1..626	615/626 (98%) 616/626 (98%)	0.0
AAR60019	Tissue-binding hybrid protein - *Homo sapiens*, 1336 aa. [WO9416085-A, 21-JUL-1994]	210..644 910..1336	416/435 (95%) 417/435 (95%)	0.0
AAB54135	Human pancreatic cancer antigen protein sequence SEQ ID NO:587 - *Homo sapiens*, 360 aa. [WO200055320-A1, 21-SEP-2000]	1..307 22..328	301/307 (98%) 301/307 (98%)	e-176

In a BLAST search of public sequence datbases, the NOV9a protein was found to have homology to the proteins shown in the BLASTP data in Table 9E.

Table 9E. Public BLASTP Results for NOV9a				
Protein Accession Number	Protein/Organism/Length	NOV9a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
FGHUA	fibrinogen alpha chain precursor, short splice form [validated] - human. 644 aa.	1..644 1..644	644/644 (100%) 644/644 (100%)	0.0
P02671	Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A] - *Homo sapiens* (Human), 866 aa.	1..641 1..645	634/645 (98%) 635/645 (98%)	0.0
P02672	Fibrinogen alpha chain [Contains: Fibrinopeptide A] - *Bos taurus* (Bovine). 596 aa (fragment).	20..644 4..596	375/633 (59%) 442/633 (69%)	0.0
Q99K47	Fibrinogen A alpha polypeptide - *Mus musculus* (Mouse), 557 aa.	1..634 1..557	371/637 (58%) 436/637 (68%)	0.0
P06399	Fibrinogen alpha/alpha-E chain precursor - *Rattus norvegicus* (Rat), 782 aa.	1..626 1..544	359/629 (57%) 428/629 (67%)	0.0

PFam analysis predicts that the NOV9a protein contains the domains shown in Table 9F.

Table 9F. Domain Analysis of NOV9a			
Pfam Domain	NOV9a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 10.

The NOV10 clone was analyzed, and the nucleotide and encoded polypeptide sequences are shown in Table 10A.

Table 10A. NOV10 Sequence Analysis		
SEQ ID NO: 37	730 bp	

NOV10a, CG137882-01 DNA Sequence	ATGCGAACACAAGTATATGAGGGGTTGTGTAAAAATTATTTTTCTCTTGCTGTACTACAA AGAGATAGAATCAAACTGCTTTTTTTCGACATACTGGTTTTTCTTTCTGTTTTTCTTCTC TTTCTTCTATTTCTTGTGGATATTATGGCTAATAACACAACAAGTTTAGGGAGTCCATGG CCAGAAAACTTTTGGGAGGACCTTATCATGTCCTTCACTGTATCCATGGCAATCGGGCTG GTACTTGGAGGATTTATTTGGGCTGTGTTCATTTGTCTGTCTCGAAGAAGAAGAGCCAGT GCTCCCATCTCACAGTGGAGTTCAAGCAGGAGATCTAGGTCTTCTTACACCCACGGCCTC AACAGAACTGGATTTTACCGCCACAGTGGCTGTGAACGTCGAAGCAACCTCAGCCTGGCC AGTCTCACCTTCCAGCGACAAGCTTCCCTGGAACAAGCAAATTCCTTTCCAAGAAAATCA AGTTTCAGAGCTTCTACTTTCCATCCCTTTCTGCAATGTCCACCACTTCCTGTGGAAACT GAGAGTCAGCTGGTGACTCTCCCTTCTTCCAATATCTCTCCCACCATCAGCACTTCCCAC AGTCTGAGCCGTCCTGACTACTGGTCCAGTAACAGTCTTCGAGTGGGCCTTTCAACACCG CCCCCACCTGCCTATGAGTCCATCATCAAGGCATTCCCAGATTCCTGAGTAGGGTGGCTT TTGGTTTTTG
	ORF Start: ATG at 1		ORF Stop: TGA at 706
	SEQ ID NO: 38	235 aa	MW at 26592.1kD
NOV10a, CG137882-01 Protein Sequence	MRTQVYEGLCKNYFSLAVLQRDRIKLLFFDILVFLSVFLLFLLFLVDIMANNTTSLGSPW PENFWEDLIMSFTVSMAIGLVLGGFIWAVFICLSRRRRASAPISQWSSSRRSRSSYTHGL NRTGFYRHSGCERRSNLSLASLTFQRQASLEQANSFPRKSSFRASTFHPFLQCPPLPVET ESQLVTLPSSNISPTISTSHSLSRPDYWSSNSLRVGLSTPPPPAYESIIKAFPDS
	SEQ ID NO: 39	630 bp	
NOV10b, CG137882-02 DNA Sequence	ATGCGAACACAAGTATATGAGGGGTTGTGTAAAAATTATTTTTCTCTTGCTGTACTACAA AGAGATAGAATCAAACTGCTTTTTTTCGACATACTGGTTTTTCTTTCTGTTTTTCTTCTC TTTCTTCTATTTCTTGTGGATATTATGGCTAATAACACAACAAGTTTAGGGAGTCCATGG CCAGAAAACTTTTGGGAGGACCTTATCATGTCCTTCACTGTATCCATGGCAATCGGGCTG GTTCTTGGAGGATTTATTTGGGCTGTGTTCATTTGTCTGTCTCGAAGAAGAAGAGCCAGT GCTCCCATCTCACAGTGGAGTTCAAGCAGGAGATCTAGGTCTTCTTACACCCACGGCCTC AACAGAACTGGATTTTACCGCCACAGTGGCTGTGAACGTCGAAGCAACCTCAGCCTGGCC AGTCTCACCTTCCAGCGACAAGCTTCCCTGGAACAAGCAAATTCCTTTCCAATATCTCTC CCACCATCAGCACTTCCCACAGTCTGAGCCGTCCTGACTACTGGTCCAGTAACAGTCTTC GAGTGGGCCTTTCAACACCGCCCCCACCTGCCTATGAGTCCATCATCAAGGCATTCCCAG ATTCCTGAGTAGGGTGGCTTTTGGTTTTTG
	ORF Start: ATG at 1		ORF Stop: TGA at 505
	SEQ ID NO: 40	168 aa	MW at 19141.9kD
NOV10b, CG137882-02 Protein Sequence	MRTQVYEGLCKNYFSLAVLQRDRIKLLFFDILVFLSVFLLFLLFLVDIMANNTTSLGSPW PENFWEDLIMSFTVSMAIGLVLGGFIWAVFICLSRRRRASAPISQWSSSRRSRSSYTHGL NRTGFYRHSGCERRSNLSLASLTFQRQASLEQANSFPISLPPSALPTV

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 10B.

Table 10B. Comparison of NOV10a against NOV10b.		
Protein Sequence	NOV10a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV10b	1..157 1..157	125/157 (79%) 125/157 (79%)

Further analysis of the NOV10a protein yielded the following properties shown in Table 10C.

Table 10C. Protein Sequence Properties NOV10a

PSort analysis:	0.6000 probability located in nucleus; 0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	Cleavage site between residues 51 and 52

A search of the NOV10a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 10D.

Table 10D. Geneseq Results for NOV10a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV10a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAY59671	Secreted protein 108-006-5-0-C2-FL - *Homo sapiens*, 187 aa. [WO9940189-A2, 12-AUG-1999]	49..235 1..187	187/187 (100%) 187/187 (100%)	e-107
AAE01707	Human gene 5 encoded secreted protein HHBCS39, SEQ ID NO:119 - *Homo sapiens*, 166 aa. [WO200134767-A2, 17-MAY-2001]	70..235 1..166	166/166 (100%) 166/166 (100%)	1e-92
AAE01676	Human gene 5 encoded secreted protein HHBCS39, SEQ ID NO:88 - *Homo sapiens*, 166 aa. [WO200134767-A2, 17-MAY-2001]	70..235 1..166	166/166 (100%) 166/166 (100%)	1e-92
AAY65073	Human 5' EST related polypeptide SEQ ID NO:1234 - *Homo sapiens*, 59 aa. [WO9953051-A2, 21-OCT-1999]	1..59 1..59	56/59 (94%) 56/59 (94%)	5e-24
AAG01373	Human secreted protein, SEQ ID NO: 5454 - *Homo sapiens*, 136 aa. [EP1033401-A2, 06-SEP-2000]	49..184 1..136	49/137 (35%) 57/137 (40%)	7e-11

In a BLAST search of public sequence datbases, the NOV10a protein was found to have homology to the proteins shown in the BLASTP data in Table 10E.

Table 10E. Public BLASTP Results for NOV10a

Protein Accession Number	Protein/Organism/Length	NOV10a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAM88866	MTLC - *Homo sapiens* (Human), 235 aa.	1..235 1..235	235/235 (100%) 235/235 (100%)	e-134
Q9H763	CDNA: FLJ21269 fis, clone COL01745 - *Homo sapiens* (Human), 235 aa.	1..235 1..235	234/235 (99%) 235/235 (99%)	e-133
CAD39158	Hypothetical protein - *Homo sapiens* (Human), 204 aa (fragment).	32..235 1..204	204/204 (100%) 204/204 (100%)	e-115
Q8TBE8	Similar to RIKEN cDNA 1110020B04 gene - *Homo sapiens* (Human), 187 aa.	49..235 1..187	186/187 (99%) 186/187 (99%)	e-105
Q8R411	MT-MC1 - *Mus musculus* (Mouse), 188 aa.	49..235 1..188	160/188 (85%) 173/188 (91%)	4e-90

PFam analysis predicts that the NOV10a protein contains the domains shown in Table 10F.

Table 10F. Domain Analysis of NOV10a			
Pfam Domain	NOV10a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 11.

The NOV11 clone was analyzed, and the nucleotide and encoded polypeptide

5   sequences are shown in Table 11A.

Table 11A. NOV11 Sequence Analysis		
	SEQ ID NO: 41	957 bp
NOV11a, CG137910-01 DNA Sequence	CATCATGCTATGGAAAAAATGGAAGAATTTGTTTGTAAGGTATGGGAAGGTCGGTGGCGA GTGATCCCTCATGATGTACTACCAGACTGGCTCAAGGATAATGACTTCCTCTTGCATGGA CACCGGCCTCCTATGCCTTCTTTCCGGGCCTGTTTTAAGAGCATTTTCAGAATACACACA GAAACAGGCAACATTTGGACACATCTCTTAGGTTGTGTATTCTTCCTGTGCCTGGGGATC TTTTATATGTTTCGCCCAAATATCTCCTTTGTGGCCCCTCTGCAAGAGAAGGTGGTCTTT GGATTATTTTTCTTAGGAGCCATTCTCTGCCTTTCTTTTTCATGGCTCTTCCACACAGTC TACTGCCACTCAGAGGGGGTCTCTCGGCTCTTCTCTAAACTGGATTACTCTGGTATTGCT CTTCTGATTATGGGAAGTTTTGTTCCTTGGCTTTATTATTCTTTCTACTGTAATCCACAA CCTTGCTTCATCTACTTGATTGTCATCTGTGTGCTGGGCATTGCAGCCATTATAGTCTCC CAGTGGGACATGTTTGCCACCCCTCAGTATCGGGGAGTAAGAGCAGGAGTGTTTTTGGGC CTAGGCCTGAGTGGAATCATTCCTACCTTGCACTATGTCATCTCGGAGGGGTTCCTTAGG GCCGCCACCATAGGGCAGATAGGCTGGTTGATGCTGATGGCCAGCCTCTACATCACAGGA GCTGCCCTGTATGCTGCCCGGATCCCCGAACGCTTTTTCCCTGGCAAATGTGACATCTGG

	TTTCACTCTCATCAGCTGTTTCATATCTTTGTGGTTGCTGGAGCTTTTGTTCACTTCCAT GGTGTCTCAAACCTCCAGGAGTTTCGTTTCATGATCGGCGGGGGCTGCAGTGAAGAGGAT GCACTGTGATACCTACCAGTCTCCAGGGACTATGACCCTAAACCAGGGCCTGCGGCA
	ORF Start: ATG at 10 | ORF Stop: TGA at 907
	SEQ ID NO: 42 | 299 aa | MW at 34157.9kD
NOV11a, CG137910-01 Protein Sequence	MEKMEEFVCKVWEGRWRVIPHDVLPDWLKDNDFLLHGHRPPMPSFRACFKSIFRIHTETG NIWTHLLGCVFFLCLGIFYMFRPNISFVAPLQEKVVFGLFFLGAILCLSFSWLFHTVYCH SEGVSRLFSKLDYSGIALLIMGSFVPWLYYSFYCNPQPCFIYLIVICVLGIAAIIVSQWD MFATPQYRGVRAGVFLGLGLSGIIPTLHYVISEGFLRAATIGQIGWLMLMASLYITGAAL YAARIPERFFPGKCDIWFHSHQLFHIFVVAGAFVHFHGVSNLQEFRFMIGGGCSEEDAL

Further analysis of the NOV11a protein yielded the following properties shown in Table 11B.

Table 11B. Protein Sequence Properties NOV11a	
PSort analysis:	0.6000 probability located in plasma membrane; 0.4000 probability located in Golgi body; 0.3000 probability located in endoplasmic reticulum (membrane); 0.3000 probability located in microbody (peroxisome)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV11a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several

5   homologous proteins shown in Table 11C.

Table 11C. Geneseq Results for NOV11a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV11a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM79290	Human protein SEQ ID NO 1952 - *Homo sapiens*, 258 aa. [WO200157190-A2, 09-AUG-2001]	42..299 1..258	256/258 (99%) 257/258 (99%)	e-154
ABB89913	Human polypeptide SEQ ID NO 2289 - *Homo sapiens*, 375 aa. [WO200190304-A2, 29-NOV-2001]	1..299 77..375	238/299 (79%) 269/299 (89%)	e-149
AAB74699	Human membrane associated protein MEMAP-5 - *Homo sapiens*, 375 aa. [WO200112662-A2, 22-FEB-2001]	1..299 77..375	238/299 (79%) 269/299 (89%)	e-149

| AAM79634 | Human protein SEQ ID NO 3280 - *Homo sapiens*, 379 aa. [WO200157190-A2, 09-AUG-2001] | 1..299 81..379 | 238/299 (79%) 269/299 (89%) | e-149 |
| AAM78650 | Human protein SEQ ID NO 1312 - *Homo sapiens*, 375 aa. [WO200157190-A2, 09-AUG-2001] | 1..299 77..375 | 238/299 (79%) 269/299 (89%) | e-149 |

In a BLAST search of public sequence datbases, the NOV11a protein was found to have homology to the proteins shown in the BLASTP data in Table 11D.

Table 11D. Public BLASTP Results for NOV11a				
Protein Accession Number	Protein/Organism/Length	NOV11a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9H737	CDNA: FLJ21432 fis, clone COL04219 - *Homo sapiens* (Human), 258 aa.	42..299 1..258	256/258 (99%) 257/258 (99%)	e-153
Q91VH1	Hypothetical 42.4 kDa protein - *Mus musculus* (Mouse), 375 aa.	1..299 77..375	238/299 (79%) 269/299 (89%)	e-149
Q96A54	Similar to CGI-45 protein (Hypothetical 42.6 kDa protein) - *Homo sapiens* (Human), 375 aa.	1..299 77..375	238/299 (79%) 269/299 (89%)	e-149
Q9Y360	CGI-45 protein - *Homo sapiens* (Human), 370 aa.	1..292 77..368	236/292 (80%) 264/292 (89%)	e-147
Q9CZA0	2810031L11Rik protein - *Mus musculus* (Mouse), 352 aa.	1..276 77..352	211/276 (76%) 236/276 (85%)	e-126

PFam analysis predicts that the NOV11a protein contains the domains shown in
5   Table 11E.

Table 11E. Domain Analysis of NOV11a			
Pfam Domain	NOV11a Match Region	Identities/ Similarities for the Matched Region	Expect Value
UPF0073	43..280	126/287 (44%) 220/287 (77%)	3.5e-125

Example 12.

The NOV12 clone was analyzed, and the nucleotide and encoded polypeptide

sequences are shown in Table 12A.

Table 12A. NOV12 Sequence Analysis			
	SEQ ID NO: 43	714 bp	
NOV12a, CG138013-01 DNA Sequence	TAACCCCAGAACATCTGGCACCTCTAACCCCAGACATCTGGCACCTCTAACCCCAGACAT CTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCCCCTGCTCTGGGGGAGGGAG AGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGACGGTGCAGGAA GGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATTTACCCT GGCCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCCA GTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTC CTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGAT GCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCAC CGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAGGCACC CTGGAGTCCGGCTGCCCCCAGAATCTGACCCACTCCTCAGTGGGGGAAGGAGAGCTCCAG TATGCATCCCTCAGCTTCCAGATGGTGAAGCCTTGGGACTCACGGGGACAGGAGGCCACT GACACCGAGTACTCGGAGATCAAGATCCACAGATGAGAAACTGCAGAGACTCAC		
	ORF Start: ATG at 82		ORF Stop: TGA at 694
	SEQ ID NO: 44	204 aa	MW at 23190.0kD
NOV12a, CG138013-01 Protein Sequence	MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGY WFREGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFR MEKGSIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTHSSVGEGELQYASLSFQ MVKPWDSRGQEATDTEYSEIKIHR		

Further analysis of the NOV12a protein yielded the following properties shown in

5   Table 12B.

Table 12B. Protein Sequence Properties NOV12a	
PSort analysis:	0.4170 probability located in lysosome (lumen); 0.3700 probability located in outside; 0.2303 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane)
SignalP analysis:	Cleavage site between residues 18 and 19

A search of the NOV12a protein against the Geneseq database, a proprietary

database that contains sequences published in patents and patent publication, yielded several

homologous proteins shown in Table 12C.

Table 12C. Geneseq Results for NOV12a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV12a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value

AAM49113	Human dendritic cell membrane protein Siglec-9 - *Homo sapiens*, 463 aa. [JP2001352977-A, 25-DEC-2001]	1..165 1..165	164/165 (99%) 164/165 (99%)	5e-97
AAU87079	Sialic acid-binding Ig-related lectin, Siglec-BMS-L5a - *Homo sapiens*, 463 aa. [WO200208257-A2, 31-JAN-2002]	1..165 1..165	164/165 (99%) 164/165 (99%)	5e-97
AAB29186	OB binding protein like protein #1 - *Homo sapiens*, 444 aa. [WO200053747-A1, 14-SEP-2000]	1..165 31..195	164/165 (99%) 164/165 (99%)	5e-97
AAB66137	Protein of the invention #49 - Unidentified, 463 aa. [WO200078961-A1, 28-DEC-2000]	1..165 1..165	164/165 (99%) 164/165 (99%)	5e-97
AAB87568	Human PRO1302 - *Homo sapiens*, 463 aa. [WO200116318-A2, 08-MAR-2001]	1..165 1..165	164/165 (99%) 164/165 (99%)	5e-97

In a BLAST search of public sequence datbases, the NOV12a protein was found to have homology to the proteins shown in the BLASTP data in Table 12D.

Table 12D. Public BLASTP Results for NOV12a

Protein Accession Number	Protein/Organism/Length	NOV12a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAF87223	Sialic acid-binding immunoglobulin-like lectin-9 - *Homo sapiens* (Human), 463 aa.	1..165 1..165	164/165 (99%) 164/165 (99%)	1e-96
Q9Y336	OB binding protein-like protein (Sialic acid-binding lectin) - *Homo sapiens* (Human), 463 aa.	1..165 1..165	164/165 (99%) 164/165 (99%)	1e-96
Q9BYI9	FOAP-9 - *Homo sapiens* (Human), 463 aa.	1..165 1..165	163/165 (98%) 164/165 (98%)	4e-96
Q9Y286	QA79 membrane protein, allelic variant AIRM-1B precursor - *Homo sapiens* (Human), 467 aa.	1..165 2..169	132/169 (78%) 138/169 (81%)	3e-68

| Q9Y502 | QA79 membrane protein, splice product AIRM-2 precursor - *Homo sapiens* (Human), 374 aa. | 1..140 2..144 | 109/144 (75%) 115/144 (79%) | 6e-55 |

PFam analysis predicts that the NOV12a protein contains the domains shown in

Table 12E.

Table 12E. Domain Analysis of NOV12a

Pfam Domain	NOV12a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 13.

The NOV13 clone was analyzed, and the nucleotide and encoded polypeptide

5   sequences are shown in Table 13A.

Table 13A. NOV13 Sequence Analysis

	SEQ ID NO: 45	1240 bp	
NOV13a, CG138074-01 DNA Sequence	GGTCACTACGTGCTCTGGCCCCTCCACCTCCTGGGTCAAAGCACCCAAGGCAGGGCTGAG GAGGTTGGGCCAGAACCGGTTGGCGGGCAGGTGGGCACATTGTCAGAGATGGCTATCAGC CTCCTCTCCCTTCTTTCTCTGTTGCAGCTGCCTTGGGGTGCGGTGCAGGGGTCCAGAGCC ATTTCGGACCTGTTACTACTGGGCCTCACAGGTGGCCTGACTCTGTTACTGCTCCTGACA CTGCTGGCCTTTGCCGGGTACTCAGGGCTGTTGGCTGGGGTGGCAGTGAGTGCCGGCTCA CCCCCCATCCGGCTCACCCCCCATCCCTACAAGTTCCATGTGGAGCCCTATGGTGAGACT GGGTGGCTTTTTCACCAGAGCTGCAGCATCTCCCCCAAGCTCTGCTCCATCGCTGTCCAC GTTCCTCTTGGCAAGTGCTGTTGTGTCCTGGGCAGCCTCCTGAGTGAAGGTGAGGAATCT CCCTCCCCTGAGCTCATCCACATCTACCAGAAATTTGACTTCAAGGCATTCTCCTTCCAG GCACCCAGCCACGTGGTGACAGCCACCTTCCCCTACACCACCATGCTGTCCATCTGGGTG GCTGCCTGCCATATCCATTCTGCCTTGGACACCTACATCAAGGGAACTGACATGATGAGT GACACGAGTTCTGGAAGCTTGGAGGTGAGCCCTGGTAGCCGGGAGACTTCATTTGCTACC GTGTCACCTGGGGAGAGCGGCCGCGGCTGGGAGGATGGTGACACCTGCAGTGAGTGCAGC TGCAGAGAGTCAGGTGCCAGCGGCTCCTCTTTTGAGGAGCTGGACCTGGAGGGTGAGGGG CCCTTGGAGGAACCACGGCTGGACCCTGAGACTGAGCCCCTGGGGGCTACCAAGTGGCCC TGAGAGCCCAGTACCCTGAGAAGGGCAAGGAGTAACCCATGACCAGCCCCCTCCTGCGGG GCAGGGCTGCGGAACCGAGCAGACTCTCCAGCCATCTTCCTCCTTCTTCTGGGGGCGAGG GGTTCCCAGGGGACGTAACTCCCCCTGCTCTAGGCCTCTTGTGAAGCCTTCTCCTCACTG TCCTTTAGGCTCCCAGGGCCAAAGCAGCCAAAGACTGTATCCTGCACCAGCCCTGTGGGC CGACACTCCTGTTGTATCTCTTTTTCAGACTGTCACTGGAGCTTCCAGGACCCAGAATAA AGCCAATGACTTACTTGTTTCAAAAAAAAAAAAAAAAAAAAG
	ORF Start: ATG at 109		ORF Stop: TGA at 901
	SEQ ID NO: 46	264 aa	MW at 28038.5kD
NOV13a, CG138074-01 Protein Sequence	MAISLLSLLSLLQLPWGAVQGSRAISDLLLLGLTGGLTLLLLLTLLAFAGYSGLLAGVAV SAGSPPIRLTPHPYKFHVEPYGETGWLFHQSCSISPKLCSIAVHVPLGKCCCVLGSLLSE GEESPSPELIHIYQKFDFKAFSFQAPSHVVTATFPYTTMLSIWVAACHIHSALDTYIKGT DMMSDTSSGSLEVSPGSRETSFATVSPGESGRGWEDGDTCSECSCRESGASGSSFEELDL EGEGPLEEPRLDPETEPLGATKWP

Further analysis of the NOV13a protein yielded the following properties shown in
Table 13B.

Table 13B. Protein Sequence Properties NOV13a	
PSort analysis:	0.4600 probability located in plasma membrane; 0.1197 probability located in microbody (peroxisome); 0.1000 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	Cleavage site between residues 50 and 51

A search of the NOV13a protein against the Geneseq database, a proprietary
database that contains sequences published in patents and patent publication, yielded several
homologous proteins shown in Table 13C.

Table 13C. Geneseq Results for NOV13a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV13a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE06730	Human CASB765 protein - *Homo sapiens*, 311 aa. [WO200157077-A1, 09-AUG-2001]	25..264 1..311	208/318 (65%) 215/318 (67%)	e-100
AAU81960	Human PRO536 - *Homo sapiens*, 313 aa. [WO200109327-A2, 08-FEB-2001]	25..263 1..301	174/302 (57%) 187/302 (61%)	8e-79
AAB65173	Human PRO536 (UNQ337) protein sequence SEQ ID NO:97 - *Homo sapiens*, 313 aa. [WO200073454-A1, 07-DEC-2000]	25..263 1..301	174/302 (57%) 187/302 (61%)	8e-79
AAB94830	Human protein sequence SEQ ID NO:15991 - *Homo sapiens*, 313 aa. [EP1074617-A2, 07-FEB-2001]	25..263 1..301	174/302 (57%) 187/302 (61%)	8e-79
AAU12370	Human PRO536 polypeptide sequence - *Homo sapiens*, 313 aa. [WO200140466-A2, 07-JUN-2001]	25..263 1..301	174/302 (57%) 187/302 (61%)	8e-79

In a BLAST search of public sequence datbases, the NOV13a protein was found to
have homology to the proteins shown in the BLASTP data in Table 13D.

Table 13D. Public BLASTP Results for NOV13a				
Protein Accession Number	Protein/Organism/Length	NOV13a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q99LS5	Similar to putative secreted protein (Unknown) (Protein for MGC:7091) - *Mus musculus* (Mouse), 309 aa.	27..259 3..296	173/294 (58%) 188/294 (63%)	2e-81
Q9D7D9	Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310012P03, full insert sequence - *Mus musculus* (Mouse), 309 aa.	27..259 3..296	172/294 (58%) 187/294 (63%)	1e-80
Q9Y6I9	Putative secreted protein ZSIG11 precursor - *Homo sapiens* (Human), 313 aa.	25..263 1..301	174/302 (57%) 187/302 (61%)	2e-78
CAC25002	Sequence 46 from Patent WO0100806 precursor - *Homo sapiens* (Human), 312 aa.	25..263 1..300	173/302 (57%) 186/302 (61%)	2e-76
Q9UKD7	Hypothetical 9.7 kDa protein - *Homo sapiens* (Human), 93 aa.	183..263 1..81	67/81 (82%) 69/81 (84%)	4e-30

PFam analysis predicts that the NOV13a protein contains the domains shown in Table 13E.

Table 13E. Domain Analysis of NOV13a			
Pfam Domain	NOV13a Match Region	Identities/ Similarities for the Matched Region	Expect Value

Example 14.

The NOV14 clone was analyzed, and the nucleotide and encoded polypeptide

5   sequences are shown in Table 14A.

Table 14A. NOV14 Sequence Analysis			
	SEQ ID NO: 47	843 bp	
NOV14a, CG138573-01 DNA Sequence	GGGGTGGAGTGGGGTGTCATTTCCATCAAGTGTGCAGCATGGGTCTCTCTGTAGCAGGCC ATGGCATGCTGGTGGCCGCTCCTGCTAGAGCTGTGGACAGTCATGCCCACCTGGGCTGGG GACGAGCTGCTCAACATCTGCATGAATGCCAAACACCACAAGAGAGTGCCCAGCCCAGAA GACAAGCTCTATGAGGAGTGCATCCCCTGGAAGGACAATGCCTGCTGCACCCTCACGACA AGCTGGGAAGCCCATCTGGATGTATCCCCACTCTACAACTTCAGCCTGTTTCACTGTGGA		